GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 22, 2005, 06:30:09 ; Search time 57 Seconds
(without alignments)
89.838 Million cell updates/sec

Title: US-10-009-809-2
Perfect score: 57
Sequence: 1 KNNLKDCGLF 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	57	100.0	53	2	Q922Y6	Q922y6 mus musculu
2	57	100.0	132	2	Q8JZT4	Q8jzt4 mus musculu
3	57	100.0	157	2	Q6LCB5	Q6lcb5 homo sapien
4	57	100.0	301	2	Q9Y206	Q9y206 hydra magni
5	57	100.0	339	2	Q8IZ71	Q8iz71 homo sapien
6	57	100.0	347	2	Q7ZWI5	Q7zwi5 brachydanio
7	57	100.0	353	1	GBI1_BOVIN	P63097 bos taurus
8	57	100.0	353	1	GBI1_CAVPO	P38401 cavia porce
9	57	100.0	353	1	GBI1_CHICK	P50146 gallus gall
10	57	100.0	353	1	GBI1_HUMAN	P63096 homo sapien
11	57	100.0	353	1	GBI1_ORYLA	P87383 oryzias lat
12	57	100.0	353	1	GBI1_RAT	P10824 rattus norv
13	57	100.0	353	1	GBI1_XENLA	P27044 xenopus lae
14	57	100.0	353	1	GBI_ASTPE	P30676 asterina pe
15	57	100.0	353	1	GBI_HELTI	P51876 helisoma tr
16	57	100.0	353	1	GBI_LYMST	P30682 lymnaea sta
17	57	100.0	354	1	GBI2_CANFA	P38400 canis famil
18	57	100.0	354	1	GBI2_CAVPO	P38402 cavia porce
19	57	100.0	354	1	GBI2_CHICK	P50147 gallus gall
20	57	100.0	354	1	GBI2_HUMAN	P04899 homo sapien
21	57	100.0	354	1	GBI2_MOUSE	P08752 mus musculu
22	57	100.0	354	1	GBI2_ORYLA	O13055 oryzias lat
23	57	100.0	354	1	GBI2_RAT	P04897 rattus norv
24	57	100.0	354	1	GBI_HOMAM	P41776 homarus ame
25	57	100.0	354	2	Q8TAN5	Q8tan5 homo sapien
26	57	100.0	354	2	Q9UGA4	Q9uga4 homo sapien
27	57	100.0	354	2	Q8WP45	Q8wp45 halocynthia
28	57	100.0	354	2	Q8WSS1	Q8wss1 ciona intes
29	57	100.0	354	2	Q8WSS2	Q8wss2 ciona intes
30	57	100.0	354	2	Q6QM16	Q6qm16 lytechinus
31	57	100.0	354	2	Q6QM17	Q6qm17 strongyloce
32	57	100.0	354	2	Q9NL94	Q9nl94 octopus vul
33	57	100.0	354	2	Q7T3D3	Q7t3d3 brachydanio
34	57	100.0	355	2	Q96C71	Q96c71 homo sapien
35	57	100.0	355	2	Q6P1C0	Q6p1c0 mus musculu
36	57	100.0	355	2	Q6P3M7	Q6p3m7 xenopus tro
37	57	100.0	355	2	Q6TNT8	Q6tnt8 brachydanio
38	57	100.0	355	2	Q9W6A4	Q9w6a4 squalus aca
39	57	100.0	357	2	Q7Q6E0	Q7q6e0 anopheles g
40	57	100.0	377	2	Q7ZW82	Q7zw82 brachydanio
41	54	94.7	82	2	Q8QGY6	Q8qgy6 fugu rubrip
42	51	89.5	47	2	Q8QGY9	Q8qgy9 fugu rubrip
43	51	89.5	157	2	Q8BSY7	Q8bsy7 mus musculu
44	51	89.5	343	2	Q9D7B3	Q9d7b3 mus musculu
45	51	89.5	349	1	GBT1_BOVIN	P04695 bos taurus

ALIGNMENTS

RESULT 1
Q922Y6
ID Q922Y6 PRELIMINARY; PRT; 53 AA.
AC Q922Y6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Gnai2 protein (Fragment).
GN Name=Gnai2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC006695; AAH06695.1; -.
DR HSSP; P10824; 1GDD.
DR MGD; MGI:95772; Gnai2.
DR GO; GO:0003924; F:GTPase activity; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007213; P:acetylcholine receptor signaling, muscarini. . .; IMP.
DR GO; GO:0007193; P:G-protein signaling, adenylate cyclase inhi. . .; IMP.
DR GO; GO:0008016; P:regulation of heart rate; IMP.
DR Pfam; PF00503; G-alpha; 1.
FT NON_TER 1 1
SQ SEQUENCE 53 AA; 6220 MW; 6574BE1F71B8B4E4 CRC64;

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  Query Match             100.0%;  Score 57;  DB 2;  Length 53;
  Best Local Similarity   100.0%;  Pred. No. 0.0039;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db         44 KNNLKDCGLF 53


RESULT 2
Q8JZT4
ID   Q8JZT4      PRELIMINARY;      PRT;   132 AA.
AC   Q8JZT4;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Gnai2 protein.
GN   Name=Gnai2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Salivary gland;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Salivary gland;
RA   Strausberg R.;
RL   Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC037130; AAH37130.1; -.
DR   HSSP; P10824; 1AGR.
DR   MGD; MGI:95772; Gnai2.
DR   GO; GO:0003924; F:GTPase activity; TAS.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0007213; P:acetylcholine receptor signaling, muscarini. . .; IMP.
DR   GO; GO:0007193; P:G-protein signaling, adenylate cyclase inhi. . .; IMP.
DR   GO; GO:0008016; P:regulation of heart rate; IMP.
DR   InterPro; IPR001019; Gprotein_alpha.
DR   InterPro; IPR001408; Gprotein_alphaI.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00441; GPROTEINAI.
DR   SMART; SM00275; G_alpha; 1.
SQ   SEQUENCE   132 AA;  15289 MW;  064DCD1E011C3C4C CRC64;

  Query Match             100.0%;  Score 57;  DB 2;  Length 132;
  Best Local Similarity   100.0%;  Pred. No. 0.01;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        123 KNNLKDCGLF 132


RESULT 3
Q6LCB5
ID   Q6LCB5      PRELIMINARY;      PRT;   157 AA.
AC   Q6LCB5;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   WUGSC:H_LUCA15.1 protein (Fragment).
GN   Name=WUGSC:H_LUCA15.1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Waterston R.;
RL   Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U73166; AAD12230.1; -.
DR   HSSP; P10824; 1AS3.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR001019; Gprotein_alpha.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   SMART; SM00275; G_alpha; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   157 AA;  18241 MW;  E420341B2294B81C CRC64;

  Query Match             100.0%;  Score 57;  DB 2;  Length 157;
  Best Local Similarity   100.0%;  Pred. No. 0.012;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        148 KNNLKDCGLF 157


RESULT 4
Q9Y206
ID   Q9Y206      PRELIMINARY;      PRT;   301 AA.
AC   Q9Y206;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   G protein a subunit 4 (Fragment).
OS   Hydra magnipapillata (Hydra).
OC   Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
OC   Hydridae; Hydra.
OX   NCBI_TaxID=6085;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99246375; PubMed=10229568;
RA   Suga H., Koyanagi M., Hoshiyama D., Ono K., Iwabe N., Kuma K.,
RA   Miyata T.;
RT   "Extensive gene duplication in the early evolution of animals before
RT   the parazoan-eumetazoan split demonstrated by G proteins and protein
RT   tyrosine kinases from sponge and hydra.";
RL   J. Mol. Evol. 48:646-653(1999).
DR   EMBL; AB006542; BAA81696.1; -.
DR   HSSP; P10824; 1BOF.
DR   GO; GO:0005525; F:GTP binding; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR001019; Gprotein_alpha.
DR   InterPro; IPR001408; Gprotein_alphaI.
DR   InterPro; IPR011025; Transducn_insert.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   PRINTS; PR00441; GPROTEINAI.
DR   SMART; SM00275; G_alpha; 1.
FT   NON_TER       1       1
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SQ   SEQUENCE   301 AA;  34701 MW;  DEE4681C554F2E3E CRC64;

  Query Match             100.0%;  Score 57;  DB 2;  Length 301;
  Best Local Similarity   100.0%;  Pred. No. 0.024;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        292 KNNLKDCGLF 301


RESULT 5
Q8IZ71
ID   Q8IZ71      PRELIMINARY;      PRT;   339 AA.
AC   Q8IZ71;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   GNAI2 protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Breast;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Breast;
RA   Strausberg R.;
RL   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC016995; AAH16995.1; -.
DR   HSSP; P10824; 1AS3.
DR   GO; GO:0005525; F:GTP binding; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR001019; Gprotein_alpha.
DR   InterPro; IPR001408; Gprotein_alphaI.
DR   InterPro; IPR011025; Transducn_insert.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   PRINTS; PR00441; GPROTEINAI.
DR   ProDom; PD000281; Gprotein_alpha; 1.
DR   SMART; SM00275; G_alpha; 1.
SQ   SEQUENCE   339 AA;  38472 MW;  F14AB734881535C5 CRC64;

  Query Match             100.0%;  Score 57;  DB 2;  Length 339;
  Best Local Similarity   100.0%;  Pred. No. 0.027;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        330 KNNLKDCGLF 339


RESULT 6
Q7ZWI5
ID   Q7ZWI5      PRELIMINARY;      PRT;   347 AA.
AC   Q7ZWI5;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Guanine nucleotide-binding protein Gi2 alpha-subunit.
GN   Name=gnai2;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Whole body;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Whole body;
RA   Strausberg R.;
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC049343; AAH49343.1; -.
DR   HSSP; P10824; 1AS3.
DR   ZFIN; ZDB-GENE-030131-5861; gnai2.
DR   GO; GO:0005525; F:GTP binding; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR001019; Gprotein_alpha.
DR   InterPro; IPR001408; Gprotein_alphaI.
DR   InterPro; IPR011025; Transducn_insert.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   PRINTS; PR00441; GPROTEINAI.
DR   ProDom; PD000281; Gprotein_alpha; 1.
DR   SMART; SM00275; G_alpha; 1.
SQ   SEQUENCE   347 AA;  39596 MW;  A04C87DBC919348C CRC64;

  Query Match             100.0%;  Score 57;  DB 2;  Length 347;
  Best Local Similarity   100.0%;  Pred. No. 0.027;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
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Db        338 KNNLKDCGLF 347


RESULT 7
GBI1_BOVIN
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ID   GBI1_BOVIN     STANDARD;      PRT;   353 AA.
AC   P63097; P04898; P11015; P31871;
DT   13-AUG-1987 (Rel. 05, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Guanine nucleotide-binding protein G(i), alpha-1 subunit (Adenylate
DE   cyclase-inhibiting G alpha protein).
GN   Name=GNAI1;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86136587; PubMed=2419165; DOI=10.1016/0014-5793(86)80347-7;
RA   Nukada T., Tanabe T., Takahashi H., Noda M., Haga K., Haga T.,
RA   Ichiyama A., Kangawa K., Hiranaga M., Matsuo H., Numa S.;
RT   "Primary structure of the alpha-subunit of bovine adenylate cyclase-
RT   inhibiting G-protein deduced from the cDNA sequence.";
RL   FEBS Lett. 197:305-310(1986).
RN   [2]
RP   SEQUENCE OF 105-353 FROM N.A.
RX   MEDLINE=87017009; PubMed=3094012;
RA   Michel T., Winslow J.W., Smith J.A., Seidman J.G., Neer E.J.;
RT   "Molecular cloning and characterization of cDNA encoding the GTP-
RT   binding protein alpha i and identification of a related protein, alpha
RT   h.";
RL   Proc. Natl. Acad. Sci. U.S.A. 83:7663-7667(1986).
CC   -!- FUNCTION: Guanine nucleotide-binding proteins (G proteins) are
CC       involved as modulators or transducers in various transmembrane
CC       signaling systems. The G(i) proteins are involved in hormonal
CC       regulation of adenylate cyclase: they inhibit the cyclase in
CC       response to beta-adrenergic stimuli.
CC   -!- SUBUNIT: G proteins are composed of 3 units; alpha, beta and
CC       gamma. The alpha chain contains the guanine nucleotide binding
CC       site.
CC   -!- SIMILARITY: Belongs to the G-alpha family. Subfamily 1
CC       (G(i/o/t/z)).
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X03642; CAA27288.1; -.
DR   EMBL; M14207; AAA30561.1; -.
DR   PIR; A23631; RGBOI1.
DR   GO; GO:0005834; C:heterotrimeric G-protein complex; TAS.
DR   GO; GO:0005886; C:plasma membrane; TAS.
DR   GO; GO:0003927; F:heterotrimeric G-protein GTPase activity; TAS.
DR   InterPro; IPR001019; Gprotein_alpha.
DR   InterPro; IPR001408; Gprotein_alphaI.
DR   InterPro; IPR011025; Transducn_insert.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   PRINTS; PR00441; GPROTEINAI.
KW   ADP-ribosylation; GTP-binding; Lipoprotein; Multigene family;
KW   Myristate; Palmitate; Transducer.
FT   INIT_MET      0      0       By similarity.
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   LIPID         2      2       S-palmitoyl cysteine (By similarity).
FT   NP_BIND      39     46       GTP (By similarity).
FT   NP_BIND     199    203       GTP (By similarity).
FT   NP_BIND     268    271       GTP (By similarity).
FT   MOD_RES     177    177       ADP-ribosylarginine (by cholera toxin).
FT   MOD_RES     350    350       ADP-ribosylcysteine (by pertussis toxin).
FT   CONFLICT    112    112       A -> S (in Ref. 2).
FT   CONFLICT    329    329       K -> N (in Ref. 2).
FT   CONFLICT    336    336       D -> E (in Ref. 2).
SQ   SEQUENCE   353 AA;  40230 MW;  B456C4E189530A6D CRC64;

  Query Match             100.0%;  Score 57;  DB 1;  Length 353;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        344 KNNLKDCGLF 353


RESULT 8
GBI1_CAVPO
ID   GBI1_CAVPO     STANDARD;      PRT;   353 AA.
AC   P38401;
DT   01-OCT-1994 (Rel. 30, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Guanine nucleotide-binding protein G(i), alpha-1 subunit (Adenylate
DE   cyclase-inhibiting G alpha protein).
GN   Name=GNAI1;
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Hartley; TISSUE=Lung;
RX   MEDLINE=93129640; PubMed=1482697; DOI=10.1016/0167-4889(92)90009-Z;
RA   Sakanaka C., Izumi T., Nakamura M., Honda Z.-I., Watanabe T.,
RA   Minami M., Mutoh H., Bito H., Seyama Y., Ui M., Shimizu T.;
RT   "Three types of Gi alpha protein of the guinea-pig lung: cDNA cloning
RT   and analysis of their tissue distribution.";
RL   Biochim. Biophys. Acta 1175:61-66(1992).
CC   -!- FUNCTION: Guanine nucleotide-binding proteins (G proteins) are
CC       involved as modulators or transducers in various transmembrane
CC       signaling systems. The G(i) proteins are involved in hormonal
CC       regulation of adenylate cyclase: they inhibit the cyclase in
CC       response to beta-adrenergic stimuli.
CC   -!- SUBUNIT: G proteins are composed of 3 units; alpha, beta and
CC       gamma. The alpha chain contains the guanine nucleotide binding
CC       site.
CC   -!- TISSUE SPECIFICITY: Mainly expressed in the brain, lung and
CC       kidney.
CC   -!- SIMILARITY: Belongs to the G-alpha family. Subfamily 1
CC       (G(i/o/t/z)).
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D21232; BAA04764.1; -.
DR   HSSP; P10824; 1AS3.
DR   InterPro; IPR001019; Gprotein_alpha.
DR   InterPro; IPR001408; Gprotein_alphaI.
DR   InterPro; IPR011025; Transducn_insert.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   PRINTS; PR00441; GPROTEINAI.
DR   ProDom; PD000281; Gprotein_alpha; 1.
KW   ADP-ribosylation; GTP-binding; Lipoprotein; Multigene family;
KW   Myristate; Palmitate; Transducer.
FT   INIT_MET      0      0       By similarity.
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   LIPID         2      2       S-palmitoyl cysteine (By similarity).
FT   NP_BIND      39     46       GTP (By similarity).
FT   NP_BIND     199    203       GTP (By similarity).
FT   NP_BIND     268    271       GTP (By similarity).
FT   MOD_RES     177    177       ADP-ribosylarginine (by cholera toxin).
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FT   MOD_RES     350    350       ADP-ribosylcysteine (by pertussis toxin).
SQ   SEQUENCE   353 AA;  40250 MW;  04E8C55DFB82D979 CRC64;

  Query Match             100.0%;  Score 57;  DB 1;  Length 353;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        344 KNNLKDCGLF 353


RESULT 9
GBI1_CHICK
ID   GBI1_CHICK     STANDARD;      PRT;   353 AA.
AC   P50146;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Guanine nucleotide-binding protein G(i), alpha-1 subunit (Adenylate
DE   cyclase-inhibiting G alpha protein).
GN   Name=GNAI1;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95121926; PubMed=7821803; DOI=10.1016/0378-1119(94)90449-9;
RA   Kilbourne E.J., Galper J.B.;
RT   "Cloning of cDNAs coding for the G alpha i1 and G alpha i2 G-proteins
RT   from chick brain.";
RL   Gene 150:341-344(1994).
CC   -!- FUNCTION: Guanine nucleotide-binding proteins (G proteins) are
CC       involved as modulators or transducers in various transmembrane
CC       signaling systems. The G(i) proteins are involved in hormonal
CC       regulation of adenylate cyclase: they inhibit the cyclase in
CC       response to beta-adrenergic stimuli.
CC   -!- SUBUNIT: G proteins are composed of 3 units; alpha, beta and
CC       gamma. The alpha chain contains the guanine nucleotide binding
CC       site.
CC   -!- SIMILARITY: Belongs to the G-alpha family. Subfamily 1
CC       (G(i/o/t/z)).
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L24548; AAA65066.1; -.
DR   PIR; I50237; I50237.
DR   HSSP; P10824; 1AS3.
DR   InterPro; IPR001019; Gprotein_alpha.
DR   InterPro; IPR001408; Gprotein_alphaI.
DR   InterPro; IPR011025; Transducn_insert.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   PRINTS; PR00441; GPROTEINAI.
DR   ProDom; PD000281; Gprotein_alpha; 1.
KW   ADP-ribosylation; GTP-binding; Lipoprotein; Multigene family;
KW   Myristate; Palmitate; Transducer.
FT   INIT_MET      0      0       By similarity.
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   LIPID         2      2       S-palmitoyl cysteine (By similarity).
FT   NP_BIND      39     46       GTP (By similarity).
FT   NP_BIND     199    203       GTP (By similarity).
FT   NP_BIND     268    271       GTP (By similarity).
FT   MOD_RES     177    177       ADP-ribosylarginine (by cholera toxin).
FT   MOD_RES     350    350       ADP-ribosylcysteine (by pertussis toxin).
SQ   SEQUENCE   353 AA;  40247 MW;  E1DD0C848140137C CRC64;

  Query Match             100.0%;  Score 57;  DB 1;  Length 353;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        344 KNNLKDCGLF 353


RESULT 10
GBI1_HUMAN
ID   GBI1_HUMAN     STANDARD;      PRT;   353 AA.
AC   P63096; P04898; P11015; P31871;
DT   13-AUG-1987 (Rel. 05, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Guanine nucleotide-binding protein G(i), alpha-1 subunit (Adenylate
DE   cyclase-inhibiting G alpha protein).
GN   Name=GNAI1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE OF 1-100 FROM N.A.
RX   MEDLINE=88198230; PubMed=2834384;
RA   Itoh H., Toyama R., Kozasa T., Tsukamoto T., Matsuoka M., Kaziro Y.;
RT   "Presence of three distinct molecular species of Gi protein alpha
RT   subunit. Structure of rat cDNAs and human genomic DNAs.";
RL   J. Biol. Chem. 263:6656-6664(1988).
RN   [2]
RP   SEQUENCE OF 5-353 FROM N.A.
RX   MEDLINE=87260939; PubMed=3110783;
RA   Bray P., Carter A., Guo V., Puckett C., Kamholz J., Spiegel A.,
RA   Nirenberg M.;
RT   "Human cDNA clones for an alpha subunit of Gi signal-transduction
RT   protein.";
RL   Proc. Natl. Acad. Sci. U.S.A. 84:5115-5119(1987).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Yu W., Gibbs R.A.;
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Puhl H.L. III, Ikeda S.R., Aronstam R.S.;
RT   "cDNA clones of human proteins involved in signal transduction
RT   sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 30-348 IN COMPLEX WITH RGS14.
RX   MEDLINE=21973246; PubMed=11976690; DOI=10.1038/416878a;
RA   Kimple R.J., Kimple M.E., Betts L., Sondek J., Siderovski D.P.;
RT   "Structural determinants for GoLoco-induced inhibition of nucleotide
RT   release by Galpha subunits.";
RL   Nature 416:878-881(2002).
CC   -!- FUNCTION: Guanine nucleotide-binding proteins (G proteins) are
CC       involved as modulators or transducers in various transmembrane
CC       signaling systems. The G(i) proteins are involved in hormonal
CC       regulation of adenylate cyclase: they inhibit the cyclase in
CC       response to beta-adrenergic stimuli.
CC   -!- SUBUNIT: G proteins are composed of 3 units; alpha, beta and
CC       gamma. The alpha chain contains the guanine nucleotide binding
CC       site.
CC   -!- SIMILARITY: Belongs to the G-alpha family. Subfamily 1
CC       (G(i/o/t/z)).
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; M20596; AAA35893.1; -.
DR   EMBL; M20594; AAA35893.1; JOINED.
DR   EMBL; M20595; AAA35893.1; JOINED.
DR   EMBL; M17219; AAA52581.1; -.
DR   EMBL; AF055013; AAC09361.1; -.
DR   EMBL; AF493905; AAM12619.1; -.
DR   PIR; A28318; RGHUI1.
DR   PDB; 1KJY; X-ray; A/C=29-353.
DR   Genew; HGNC:4384; GNAI1.
DR   MIM; 139310; -.
DR   GO; GO:0005834; C:heterotrimeric G-protein complex; TAS.
DR   GO; GO:0005886; C:plasma membrane; TAS.
DR   GO; GO:0003927; F:heterotrimeric G-protein GTPase activity; TAS.
DR   InterPro; IPR001019; Gprotein_alpha.
DR   InterPro; IPR001408; Gprotein_alphaI.
DR   InterPro; IPR011025; Transducn_insert.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   PRINTS; PR00441; GPROTEINAI.
KW   3D-structure; ADP-ribosylation; GTP-binding; Lipoprotein;
KW   Multigene family; Myristate; Palmitate; Transducer.
FT   INIT_MET      0      0       By similarity.
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   LIPID         2      2       S-palmitoyl cysteine (By similarity).
FT   NP_BIND      39     46       GTP (By similarity).
FT   NP_BIND     199    203       GTP (By similarity).
FT   NP_BIND     268    271       GTP (By similarity).
FT   MOD_RES     177    177       ADP-ribosylarginine (by cholera toxin).
FT   MOD_RES     350    350       ADP-ribosylcysteine (by pertussis toxin).
FT   STRAND       32     38
FT   TURN         41     42
FT   HELIX        45     55
FT   HELIX        62     65
FT   HELIX        66     68
FT   HELIX        69     89
FT   TURN         90     91
FT   TURN         97     98
FT   HELIX        99    112
FT   TURN        115    116
FT   HELIX       120    131
FT   HELIX       133    139
FT   TURN        140    141
FT   HELIX       142    144
FT   TURN        149    150
FT   HELIX       151    155
FT   TURN        156    157
FT   HELIX       158    161
FT   TURN        164    165
FT   HELIX       170    175
FT   STRAND      184    190
FT   TURN        191    192
FT   STRAND      193    199
FT   HELIX       207    214
FT   TURN        215    216
FT   STRAND      219    225
FT   HELIX       226    230
FT   TURN        235    236
FT   HELIX       241    254
FT   HELIX       256    258
FT   TURN        259    260
FT   STRAND      264    268
FT   HELIX       270    276
FT   TURN        277    279
FT   HELIX       282    284
FT   TURN        285    285
FT   TURN        287    288
FT   HELIX       295    307
FT   TURN        308    309
FT   TURN        311    315
FT   STRAND      319    322
FT   TURN        325    326
FT   HELIX       328    344
FT   TURN        345    345
SQ   SEQUENCE   353 AA;  40230 MW;  B456C4E189530A6D CRC64;

  Query Match             100.0%;  Score 57;  DB 1;  Length 353;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        344 KNNLKDCGLF 353


RESULT 11
GBI1_ORYLA
ID   GBI1_ORYLA     STANDARD;      PRT;   353 AA.
AC   P87383;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Guanine nucleotide-binding protein G(i), alpha-1 subunit (Adenylate
DE   cyclase-inhibiting G alpha protein) (Gi1 alpha subunit) (Gi alpha a).
GN   Name=GNAI1;
OS   Oryzias latipes (Medaka fish) (Japanese ricefish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC   Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
OX   NCBI_TaxID=8090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RX   MEDLINE=98055713; PubMed=9395335;
RA   Oba Y., Yoshikuni M., Tanaka M., Mita M., Nagahama Y.;
RT   "Inhibitory guanine-nucleotide-binding-regulatory protein alpha
RT   subunits in medaka (Oryzias latipes) oocytes -- cDNA cloning and
RT   decreased expression of proteins during oocyte maturation.";
RL   Eur. J. Biochem. 249:846-853(1997).
CC   -!- FUNCTION: Guanine nucleotide-binding proteins (G proteins) are
CC       involved as modulators or transducers in various transmembrane
CC       signaling systems. The G(i) proteins are involved in hormonal
CC       regulation of adenylate cyclase: they inhibit the cyclase in
CC       response to beta-adrenergic stimuli.
CC   -!- SUBUNIT: G proteins are composed of 3 units; alpha, beta and
CC       gamma. The alpha chain contains the guanine nucleotide binding
CC       site.
CC   -!- SIMILARITY: Belongs to the G-alpha family. Subfamily 1
CC       (G(i/o/t/z)).
CC   ---------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; AB001741; BAA19454.1; -.
DR   HSSP; P10824; 1AS3.
DR   InterPro; IPR001019; Gprotein_alpha.
DR   InterPro; IPR001408; Gprotein_alphaI.
DR   InterPro; IPR011025; Transducn_insert.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   PRINTS; PR00441; GPROTEINAI.
DR   ProDom; PD000281; Gprotein_alpha; 1.
DR   SMART; SM00275; G_alpha; 1.
KW   ADP-ribosylation; GTP-binding; Lipoprotein; Multigene family;
KW   Myristate; Palmitate; Transducer.
FT   INIT_MET      0      0       By similarity.
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
```

```
FT   LIPID         2      2       S-palmitoyl cysteine (By similarity).
FT   NP_BIND      39     46       GTP (By similarity).
FT   NP_BIND     199    203       GTP (By similarity).
FT   NP_BIND     268    271       GTP (By similarity).
FT   MOD_RES     177    177       ADP-ribosylarginine (by cholera toxin)
FT                                (By similarity).
FT   MOD_RES     350    350       ADP-ribosylcysteine (by pertussis toxin)
FT                                (By similarity).
SQ   SEQUENCE   353 AA;  40149 MW;  FBD5A91D0D69DFC0 CRC64;

  Query Match             100.0%;  Score 57;  DB 1;  Length 353;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        344 KNNLKDCGLF 353


RESULT 12
GBI1_RAT
ID   GBI1_RAT       STANDARD;      PRT;   353 AA.
AC   P10824;
DT   01-JUL-1989 (Rel. 11, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Guanine nucleotide-binding protein G(i), alpha-1 subunit (Adenylate
DE   cyclase-inhibiting G alpha protein).
GN   Name=Gnai1; Synonyms=Gnai-1;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88007678; PubMed=2820999;
RA   Jones D.T., Reed R.R.;
RT   "Molecular cloning of five GTP-binding protein cDNA species from rat
RT   olfactory neuroepithelium.";
RL   J. Biol. Chem. 262:14241-14249(1987).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX   MEDLINE=94353239; PubMed=8073283;
RA   Coleman D.E., Berghuis A.M., Lee E., Linder M.E., Gilman A.G.,
RA   Sprang S.R.;
RT   "Structures of active conformations of Gi alpha 1 and the mechanism of
RT   GTP hydrolysis.";
RL   Science 265:1405-1412(1994).
RN   [3]
RP   X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF HETEROTRIMER.
RX   MEDLINE=96107343; PubMed=8521505; DOI=10.1016/0092-8674(95)90220-1;
RA   Wall M.A., Coleman D.E., Lee E., Iniguez-Lluhi J.A., Posner B.A.,
RA   Gilman A.G., Sprang S.R.;
RT   "The structure of the G protein heterotrimer Gi alpha 1 beta 1 gamma
RT   2.";
RL   Cell 83:1047-1058(1995).
RN   [4]
RP   X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH RGS4.
RX   MEDLINE=97262066; PubMed=9108480; DOI=10.1016/S0092-8674(00)80204-4;
RA   Tesmer J.J.G., Berman D.M., Gilman A.G., Sprang S.R.;
RT   "Structure of RGS4 bound to AlF4-activated G(i alpha1): stabilization
RT   of the transition state for GTP hydrolysis.";
RL   Cell 89:251-261(1997).
RN   [5]
RP   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX   MEDLINE=98447508; PubMed=9772163; DOI=10.1021/bi9810306;
RA   Coleman D.E., Sprang S.R.;
RT   "Crystal structures of the G protein Gi alpha 1 complexed with GDP and
RT   Mg2+: a crystallographic titration experiment.";
RL   Biochemistry 37:14376-14385(1998).
RN   [6]
RP   X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 31-345.
RX   MEDLINE=98371012; PubMed=9705312; DOI=10.1074/jbc.273.34.21752;
RA   Posner B.A., Mixon M.B., Wall M.A., Sprang S.R., Gilman A.G.;
RT   "The A326S mutant of Gialpha1 as an approximation of the receptor-
RT   bound state.";
RL   J. Biol. Chem. 273:21752-21758(1998).
CC   -!- FUNCTION: Guanine nucleotide-binding proteins (G proteins) are
CC       involved as modulators or transducers in various transmembrane
CC       signaling systems. The G(i) proteins are involved in hormonal
CC       regulation of adenylate cyclase: they inhibit the cyclase in
CC       response to beta-adrenergic stimuli.
CC   -!- SUBUNIT: G proteins are composed of 3 units; alpha, beta and
CC       gamma. The alpha chain contains the guanine nucleotide binding
CC       site.
CC   -!- SIMILARITY: Belongs to the G-alpha family. Subfamily 1
CC       (G(i/o/t/z)).
CC   ---------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M17527; AAA40825.1; -.
DR   PIR; C27423; RGRTI1.
DR   PDB; 1AGR; X-ray; A/D=1-353.
DR   PDB; 1AS0; X-ray; @=1-353.
DR   PDB; 1AS2; X-ray; @=1-353.
DR   PDB; 1AS3; X-ray; @=1-353.
DR   PDB; 1BH2; X-ray; @=31-344.
DR   PDB; 1BOF; X-ray; @=1-353.
DR   PDB; 1CIP; X-ray; A=1-353.
DR   PDB; 1GDD; X-ray; @=1-353.
DR   PDB; 1GFI; X-ray; @=1-353.
DR   PDB; 1GG2; X-ray; A=1-353.
DR   PDB; 1GIA; X-ray; @=1-353.
DR   PDB; 1GIL; X-ray; @=1-353.
DR   PDB; 1GIT; X-ray; @=1-353.
DR   PDB; 1GP2; X-ray; A=1-353.
DR   RGD; 2713; Gnai1.
DR   InterPro; IPR001019; Gprotein_alpha.
DR   InterPro; IPR001408; Gprotein_alphaI.
DR   InterPro; IPR011025; Transducn_insert.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   PRINTS; PR00441; GPROTEINAI.
DR   ProDom; PD000281; Gprotein_alpha; 1.
KW   3D-structure; ADP-ribosylation; GTP-binding; Lipoprotein;
KW   Multigene family; Myristate; Palmitate; Transducer.
FT   INIT_MET      0      0       By similarity.
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   NP_BIND      39     46       GTP (By similarity).
FT   NP_BIND     199    203       GTP (By similarity).
FT   NP_BIND     268    271       GTP (By similarity).
FT   MOD_RES     177    177       ADP-ribosylarginine (by cholera toxin).
FT   MOD_RES     350    350       ADP-ribosylcysteine (by pertussis toxin).
FT   STRAND       32     38
FT   TURN         41     42
FT   HELIX        45     56
FT   HELIX        62     67
FT   TURN         68     68
FT   HELIX        69     90
FT   TURN         91     91
FT   TURN         97     98
FT   HELIX        99    113
FT   TURN        114    116
FT   HELIX       120    131
FT   HELIX       133    139
FT   TURN        140    141
FT   HELIX       142    144
FT   TURN        149    150
FT   HELIX       151    155
FT   TURN        156    157
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FT   HELIX       158    161
FT   TURN        162    162
FT   TURN        164    165
FT   HELIX       170    174
FT   TURN        175    175
FT   STRAND      183    190
FT   TURN        191    192
FT   STRAND      193    200
FT   HELIX       204    213
FT   TURN        215    216
FT   STRAND      219    225
FT   HELIX       226    230
FT   STRAND      232    233
FT   TURN        234    235
FT   STRAND      236    240
FT   HELIX       241    253
FT   TURN        254    254
FT   HELIX       256    258
FT   TURN        259    260
FT   STRAND      262    268
FT   HELIX       270    277
FT   TURN        278    279
FT   HELIX       282    284
FT   TURN        285    285
FT   TURN        287    288
FT   HELIX       295    307
FT   TURN        308    309
FT   TURN        313    315
FT   STRAND      318    322
FT   TURN        325    326
FT   HELIX       328    345
SQ   SEQUENCE   353 AA;  40214 MW;  B23724E187E90A6D CRC64;

  Query Match             100.0%;  Score 57;  DB 1;  Length 353;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        344 KNNLKDCGLF 353


RESULT 13
GBI1_XENLA
ID   GBI1_XENLA     STANDARD;      PRT;   353 AA.
AC   P27044;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Guanine nucleotide-binding protein G(i), alpha-1 subunit (Adenylate
DE   cyclase-inhibiting G alpha protein).
GN   Name=GNAI1;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Oocyte;
RX   MEDLINE=90346157; PubMed=2116977; DOI=10.1016/0014-5793(90)80964-K;
RA   Olate J., Martinez S., Purcell P., Jorquera H., Codina J.,
RA   Birnbaumer L., Allende J.E.;
RT   "Molecular cloning and sequence determination of four different cDNA
RT   species coding for alpha-subunits of G proteins from Xenopus laevis
RT   oocytes.";
RL   FEBS Lett. 268:27-31(1990).
CC   -!- FUNCTION: Guanine nucleotide-binding proteins (G proteins) are
CC       involved as modulators or transducers in various transmembrane
CC       signaling systems. The G(i) proteins are involved in hormonal
CC       regulation of adenylate cyclase: they inhibit the cyclase in
CC       response to beta-adrenergic stimuli.
CC   -!- SUBUNIT: G proteins are composed of 3 units; alpha, beta and
CC       gamma. The alpha chain contains the guanine nucleotide binding
CC       site.
CC   -!- SIMILARITY: Belongs to the G-alpha family. Subfamily 1
CC       (G(i/o/t/z)).
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X56089; CAA39569.1; -.
DR   PIR; S11045; RGXLI1.
DR   HSSP; P10824; 1AS3.
DR   InterPro; IPR001019; Gprotein_alpha.
DR   InterPro; IPR001408; Gprotein_alphaI.
DR   InterPro; IPR011025; Transducn_insert.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   PRINTS; PR00441; GPROTEINAI.
DR   ProDom; PD000281; Gprotein_alpha; 1.
KW   ADP-ribosylation; GTP-binding; Lipoprotein; Multigene family;
KW   Myristate; Palmitate; Transducer.
FT   INIT_MET      0      0       By similarity.
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   LIPID         2      2       S-palmitoyl cysteine (By similarity).
FT   NP_BIND      39     46       GTP (By similarity).
FT   NP_BIND     199    203       GTP (By similarity).
FT   NP_BIND     268    271       GTP (By similarity).
FT   MOD_RES     177    177       ADP-ribosylarginine (by cholera toxin).
FT   MOD_RES     350    350       ADP-ribosylcysteine (by pertussis toxin).
SQ   SEQUENCE   353 AA;  40270 MW;  6B4EE94P841B077D CRC64;

  Query Match             100.0%;  Score 57;  DB 1;  Length 353;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        344 KNNLKDCGLF 353


RESULT 14
GBI_ASTPE
ID   GBI_ASTPE      STANDARD;      PRT;   353 AA.
AC   P30676;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Guanine nucleotide-binding protein G(i), alpha subunit (Adenylate
DE   cyclase-inhibiting G alpha protein).
OS   Asterina pectinifera (Starfish).
OC   Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
OC   Asteroidea; Valvatacea; Valvatida; Asterinidae; Asterina.
OX   NCBI_TaxID=7594;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC   TISSUE=Ovary;
RX   MEDLINE=92362619; PubMed=1499560;
RA   Chiba K., Tadenuma H., Matsumoto M., Takahashi K., Katada T.,
RA   Hoshi M.;
RT   "The primary structure of the alpha subunit of a starfish guanosine-
RT   nucleotide-binding regulatory protein involved in 1-methyladenine-
RT   induced oocyte maturation.";
RL   Eur. J. Biochem. 207:833-838(1992).
CC   -!- FUNCTION: Guanine nucleotide-binding proteins (G proteins) are
CC       involved as modulators or transducers in various transmembrane
CC       signaling systems. This G protein is involved in 1-methyladenine-
CC       induced oocyte maturation.
CC   -!- SUBUNIT: G proteins are composed of 3 units; alpha, beta and
CC       gamma. The alpha chain contains the guanine nucleotide binding
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CC       site.
CC   -!- SIMILARITY: Belongs to the G-alpha family. Subfamily 1
CC       (G(i/o/t/z)).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X66378; CAA47019.1; -.
DR   PIR; S24362; S24362.
DR   HSSP; P10824; 1AS3.
DR   InterPro; IPR001019; Gprotein_alpha.
DR   InterPro; IPR001408; Gprotein_alphaI.
DR   InterPro; IPR011025; Transducn_insert.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   PRINTS; PR00441; GPROTEINAI.
DR   ProDom; PD000281; Gprotein_alpha; 1.
KW   ADP-ribosylation; Direct protein sequencing; GTP-binding; Lipoprotein;
KW   Multigene family; Myristate; Transducer.
FT   INIT_MET      0      0       By similarity.
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   NP_BIND      39     46       GTP (By similarity).
FT   NP_BIND     199    203       GTP (By similarity).
FT   NP_BIND     268    271       GTP (By similarity).
FT   MOD_RES     177    177       ADP-ribosylarginine (by cholera toxin)
FT                                (By similarity).
FT   MOD_RES     350    350       ADP-ribosylcysteine (by pertussis toxin)
FT                                (By similarity).
SQ   SEQUENCE   353 AA;  39911 MW;  C99C00415EAE226F CRC64;

  Query Match             100.0%;  Score 57;  DB 1;  Length 353;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        344 KNNLKDCGLF 353


RESULT 15
GBI_HELTI
ID   GBI_HELTI      STANDARD;      PRT;   353 AA.
AC   P51876;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Guanine nucleotide-binding protein G(i), alpha subunit (Adenylate
DE   cyclase-inhibiting G alpha protein).
OS   Helisoma trivolvis (Snail).
OC   Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC   Lymnaeoidea; Planorbidae; Helisoma.
OX   NCBI_TaxID=27815;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Oregon red; TISSUE=Central ganglion;
RX   MEDLINE=94138304; PubMed=7508312; DOI=10.1016/0928-4257(93)90006-F;
RA   Durgerian S., Bahls F., Richmond J., Doyle R.T., Larson D.D.,
RA   Haydon P.G.;
RT   "Roles for arachidonic acid and GTP-binding proteins in synaptic
RT   transmission.";
RL   J. Physiol. (Paris) 87:123-137(1993).
CC   -!- FUNCTION: Guanine nucleotide-binding proteins (G proteins) are
CC       involved as modulators or transducers in various transmembrane
CC       signaling systems.
CC   -!- SUBUNIT: G proteins are composed of 3 units; alpha, beta and
CC       gamma. The alpha chain contains the guanine nucleotide binding
CC       site.
CC   -!- SIMILARITY: Belongs to the G-alpha family. Subfamily 1
CC       (G(i/o/t/z)).
CC   ---------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L18922; AAC41538.1; -.
DR   HSSP; P10824; 1GDD.
DR   InterPro; IPR001019; Gprotein_alpha.
DR   InterPro; IPR001408; Gprotein_alphaI.
DR   InterPro; IPR011025; Transducn_insert.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   PRINTS; PR00441; GPROTEINAI.
DR   ProDom; PD000281; Gprotein_alpha; 1.
KW   ADP-ribosylation; GTP-binding; Lipoprotein; Multigene family;
KW   Myristate; Transducer.
FT   INIT_MET      0      0       By similarity.
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   NP_BIND      39     46       GTP (By similarity).
FT   NP_BIND     199    203       GTP (By similarity).
FT   NP_BIND     268    271       GTP (By similarity).
FT   MOD_RES     177    177       ADP-ribosylarginine (by cholera toxin)
FT                                (By similarity).
FT   MOD_RES     350    350       ADP-ribosylcysteine (by pertussis toxin)
FT                                (By similarity).
SQ   SEQUENCE   353 AA;  40412 MW;  19878620EECFA76A CRC64;

  Query Match             100.0%;  Score 57;  DB 1;  Length 353;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        344 KNNLKDCGLF 353


RESULT 16
GBI_LYMST
ID   GBI_LYMST      STANDARD;      PRT;   353 AA.
AC   P30682;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Guanine nucleotide-binding protein G(i), alpha subunit (Adenylate
DE   cyclase-inhibiting G alpha protein).
OS   Lymnaea stagnalis (Great pond snail).
OC   Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC   Lymnaeoidea; Lymnaeidae; Lymnaea.
OX   NCBI_TaxID=6523;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=CNS;
RX   MEDLINE=93106153; PubMed=1468550; DOI=10.1016/0014-5793(92)81474-Z;
RA   Knol J.C., Weidemann W., Planta R.J., Vreugdenhil E.,
RA   van Heerikhuizen H.;
RT   "Molecular cloning of G protein alpha subunits from the central
RT   nervous system of the mollusc Lymnaea stagnalis.";
RL   FEBS Lett. 314:215-219(1992).
CC   -!- FUNCTION: Guanine nucleotide-binding proteins (G proteins) are
CC       involved as modulators or transducers in various transmembrane
CC       signaling systems. The G(i) proteins are involved in hormonal
CC       regulation of adenylate cyclase: they inhibit the cyclase in
CC       response to beta-adrenergic stimuli.
CC   -!- SUBUNIT: G proteins are composed of 3 units; alpha, beta and
CC       gamma. The alpha chain contains the guanine nucleotide binding
CC       site.
CC   -!- SIMILARITY: Belongs to the G-alpha family. Subfamily 1
CC       (G(i/o/t/z)).
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CC   ----------------------------------------------------------------------
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; Z15095; CAA78807.1; -.
DR   PIR; S27013; S27013.
DR   HSSP; P10824; 1GDD.
DR   InterPro; IPR001019; Gprotein_alpha.
DR   InterPro; IPR001408; Gprotein_alphaI.
DR   InterPro; IPR011025; Transducn_insert.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   PRINTS; PR00441; GPROTEINAI.
DR   ProDom; PD000281; Gprotein_alpha; 1.
KW   ADP-ribosylation; GTP-binding; Lipoprotein; Multigene family;
KW   Myristate; Transducer.
FT   INIT_MET      0      0       By similarity.
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   NP_BIND      39     46       GTP (By similarity).
FT   NP_BIND     199    203       GTP (By similarity).
FT   NP_BIND     268    271       GTP (By similarity).
FT   MOD_RES     177    177       ADP-ribosylarginine (by cholera toxin)
FT                                (By similarity).
FT   MOD_RES     350    350       ADP-ribosylcysteine (by pertussis toxin)
FT                                (By similarity).
SQ   SEQUENCE   353 AA;  40355 MW;  42277D2C0958EE1F CRC64;

  Query Match             100.0%;  Score 57;  DB 1;  Length 353;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        344 KNNLKDCGLF 353


RESULT 17
GBI2_CANFA
ID   GBI2_CANFA     STANDARD;      PRT;   354 AA.
AC   P38400;
DT   01-OCT-1994 (Rel. 30, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Guanine nucleotide-binding protein G(i), alpha-2 subunit (Adenylate
DE   cyclase-inhibiting G alpha protein).
GN   Name=GNAI2;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90003652; PubMed=2477170;
RA   Holmer S.R., Stevens S., Homcy C.J.;
RT   "Tissue- and species-specific expression of inhibitory guanine
RT   nucleotide-binding proteins. Cloning of a full-length complementary
RT   DNA from canine heart.";
RL   Circ. Res. 65:1136-1140(1989).
CC   -!- FUNCTION: Guanine nucleotide-binding proteins (G proteins) are
CC       involved as modulators or transducers in various transmembrane
CC       signaling systems. The G(i) proteins are involved in hormonal
CC       regulation of adenylate cyclase: they inhibit the cyclase in
CC       response to beta-adrenergic stimuli.
CC   -!- SUBUNIT: G proteins are composed of 3 units; alpha, beta and
CC       gamma. The alpha chain contains the guanine nucleotide binding
CC       site. Interacts with UNC5B (By similarity).
CC   -!- SIMILARITY: Belongs to the G-alpha family. Subfamily 1
CC       (G(i/o/t/z)).
DR   PIR; A61031; A61031.
DR   HSSP; P10824; 1AS3.
DR   InterPro; IPR001019; Gprotein_alpha.
DR   InterPro; IPR001408; Gprotein_alphaI.
DR   InterPro; IPR011025; Transducn_insert.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   PRINTS; PR00441; GPROTEINAI.
DR   ProDom; PD000281; Gprotein_alpha; 1.
KW   ADP-ribosylation; GTP-binding; Lipoprotein; Multigene family;
KW   Myristate; Palmitate; Transducer.
FT   INIT_MET      0      0       By similarity.
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   LIPID         2      2       S-palmitoyl cysteine (By similarity).
FT   NP_BIND      39     46       GTP (By similarity).
FT   NP_BIND     200    204       GTP (By similarity).
FT   NP_BIND     269    272       GTP (By similarity).
FT   MOD_RES     178    178       ADP-ribosylarginine (by cholera toxin).
FT   MOD_RES     351    351       ADP-ribosylcysteine (by pertussis toxin).
SQ   SEQUENCE   354 AA;  40414 MW;  93A01B69AA9DBDE7 CRC64;

  Query Match             100.0%;  Score 57;  DB 1;  Length 354;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        345 KNNLKDCGLF 354


RESULT 18
GBI2_CAVPO
ID   GBI2_CAVPO     STANDARD;      PRT;   354 AA.
AC   P38402;
DT   01-OCT-1994 (Rel. 30, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Guanine nucleotide-binding protein G(i), alpha-2 subunit (Adenylate
DE   cyclase-inhibiting G alpha protein).
GN   Name=GNAI2;
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Hartley; TISSUE=Lung;
RX   MEDLINE=93129640; PubMed=1482697; DOI=10.1016/0167-4889(92)90009-Z;
RA   Sakanaka C., Izumi T., Nakamura M., Honda Z.-I., Watanabe T.,
RA   Minami M., Mutoh H., Bito H., Seyama Y., Ui M., Shimizu T.;
RT   "Three types of Gi alpha protein of the guinea-pig lung: cDNA cloning
RT   and analysis of their tissue distribution.";
RL   Biochim. Biophys. Acta 1175:61-66(1992).
CC   -!- FUNCTION: Guanine nucleotide-binding proteins (G proteins) are
CC       involved as modulators or transducers in various transmembrane
CC       signaling systems. The G(i) proteins are involved in hormonal
CC       regulation of adenylate cyclase: they inhibit the cyclase in
CC       response to beta-adrenergic stimuli.
CC   -!- SUBUNIT: G proteins are composed of 3 units; alpha, beta and
CC       gamma. The alpha chain contains the guanine nucleotide binding
CC       site. Interacts with UNC5B (By similarity).
CC   -!- TISSUE SPECIFICITY: Ubiquitously expressed. Most abundant in the
CC       lung and in the spleen.
CC   -!- SIMILARITY: Belongs to the G-alpha family. Subfamily 1
CC       (G(i/o/t/z)).
CC   ----------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
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CC   ---------------------------------------------------------------------
DR   EMBL; D21233; BAA04765.1; -.
DR   HSSP; P10824; 1AS3.
DR   InterPro; IPR001019; Gprotein_alpha.
DR   InterPro; IPR001408; Gprotein_alphaI.
DR   InterPro; IPR011025; Transducn_insert.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   PRINTS; PR00441; GPROTEINAI.
DR   ProDom; PD000281; Gprotein_alpha; 1.
KW   ADP-ribosylation; GTP-binding; Lipoprotein; Multigene family;
KW   Myristate; Palmitate; Transducer.
FT   INIT_MET      0      0       By similarity.
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   LIPID         2      2       S-palmitoyl cysteine (By similarity).
FT   NP_BIND      39     46       GTP (By similarity).
FT   NP_BIND     200    204       GTP (By similarity).
FT   NP_BIND     269    272       GTP (By similarity).
FT   MOD_RES     178    178       ADP-ribosylarginine (by cholera toxin).
FT   MOD_RES     351    351       ADP-ribosylcysteine (by pertussis toxin).
SQ   SEQUENCE   354 AA;  40408 MW;  D6C151413CC5EB91 CRC64;

  Query Match             100.0%;  Score 57;  DB 1;  Length 354;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        345 KNNLKDCGLF 354


RESULT 19
GBI2_CHICK
ID   GBI2_CHICK     STANDARD;      PRT;   354 AA.
AC   P50147;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Guanine nucleotide-binding protein G(i), alpha-2 subunit (Adenylate
DE   cyclase-inhibiting G alpha protein).
GN   Name=GNAI2;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95121926; PubMed=7821803; DOI=10.1016/0378-1119(94)90449-9;
RA   Kilbourne E.J., Galper J.B.;
RT   "Cloning of cDNAs coding for the G alpha i1 and G alpha i2 G-proteins
RT   from chick brain.";
RL   Gene 150:341-344(1994).
CC   -!- FUNCTION: Guanine nucleotide-binding proteins (G proteins) are
CC       involved as modulators or transducers in various transmembrane
CC       signaling systems. The G(i) proteins are involved in hormonal
CC       regulation of adenylate cyclase: they inhibit the cyclase in
CC       response to beta-adrenergic stimuli.
CC   -!- SUBUNIT: G proteins are composed of 3 units; alpha, beta and
CC       gamma. The alpha chain contains the guanine nucleotide binding
CC       site.
CC   -!- SIMILARITY: Belongs to the G-alpha family. Subfamily 1
CC       (G(i/o/t/z)).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L24549; AAA65067.1; -.
DR   PIR; I50238; I50238.
DR   HSSP; P10824; 1AS3.
DR   InterPro; IPR001019; Gprotein_alpha.
DR   InterPro; IPR001408; Gprotein_alphaI.
DR   InterPro; IPR011025; Transducn_insert.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   PRINTS; PR00441; GPROTEINAI.
DR   ProDom; PD000281; Gprotein_alpha; 1.
KW   ADP-ribosylation; GTP-binding; Lipoprotein; Multigene family;
KW   Myristate; Palmitate; Transducer.
FT   INIT_MET      0      0       By similarity.
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   LIPID         2      2       S-palmitoyl cysteine (By similarity).
FT   NP_BIND      39     46       GTP (By similarity).
FT   NP_BIND     200    204       GTP (By similarity).
FT   NP_BIND     269    272       GTP (By similarity).
FT   MOD_RES     178    178       ADP-ribosylarginine (by cholera toxin).
FT   MOD_RES     351    351       ADP-ribosylcysteine (by pertussis toxin).
SQ   SEQUENCE   354 AA;  40446 MW;  D9645493D9C5CC4F CRC64;

  Query Match             100.0%;  Score 57;  DB 1;  Length 354;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        345 KNNLKDCGLF 354


RESULT 20
GBI2_HUMAN
ID   GBI2_HUMAN     STANDARD;      PRT;   354 AA.
AC   P04899;
DT   13-AUG-1987 (Rel. 05, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Guanine nucleotide-binding protein G(i), alpha-2 subunit (Adenylate
DE   cyclase-inhibiting G alpha protein).
GN   Name=GNAI2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87105966; PubMed=3100330; DOI=10.1016/0014-5793(87)81428-X;
RA   Didsbury J.R., Ho Y.-S., Snyderman R.;
RT   "Human Gi protein alpha-subunit: deduction of amino acid structure
RT   from a cloned cDNA.";
RL   FEBS Lett. 211:160-164(1987).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88198230; PubMed=2834384;
RA   Itoh H., Toyama R., Kozasa T., Tsukamoto T., Matsuoka M., Kaziro Y.;
RT   "Presence of three distinct molecular species of Gi protein alpha
RT   subunit. Structure of rat cDNAs and human genomic DNAs.";
RL   J. Biol. Chem. 263:6656-6664(1988).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88068503; PubMed=3120178;
RA   Beals C.R., Wilson C.B., Perlmutter R.M.;
RT   "A small multigene family encodes Gi signal-transduction proteins.";
RL   Proc. Natl. Acad. Sci. U.S.A. 84:7886-7890(1987).
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Puhl H.L. III, Ikeda S.R., Aronstam R.S.;
RT   "cDNA clones of human proteins involved in signal transduction
RT   sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
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RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [6]
RP   SEQUENCE OF 1-38 FROM N.A.
RX   MEDLINE=88242822; PubMed=2837412; DOI=10.1016/0014-5793(88)80764-6;
RA   Weinstein L.S., Spiegel A.M., Carter A.D.;
RT   "Cloning and characterization of the human gene for the alpha-subunit
RT   of Gi2, a GTP-binding signal transduction protein.";
RL   FEBS Lett. 232:333-340(1988).
RN   [7]
RP   INTERACTION WITH UNC5B.
RX   MEDLINE=22246081; PubMed=12359238; DOI=10.1016/S0006-291X(02)02277-5;
RA   Komatsuzaki K., Dalvin S., Kinane T.B.;
RT   "Modulation of G(ialpha(2)) signaling by the axonal guidance molecule
RT   UNC5H2.";
RL   Biochem. Biophys. Res. Commun. 297:898-905(2002).
CC   -!- FUNCTION: Guanine nucleotide-binding proteins (G proteins) are
CC       involved as modulators or transducers in various transmembrane
CC       signaling systems. The G(i) proteins are involved in hormonal
CC       regulation of adenylate cyclase: they inhibit the cyclase in
CC       response to beta-adrenergic stimuli.
CC   -!- SUBUNIT: G proteins are composed of 3 units; alpha, beta and
CC       gamma. The alpha chain contains the guanine nucleotide binding
CC       site. Interacts with UNC5B.
CC   -!- SIMILARITY: Belongs to the G-alpha family. Subfamily 1
CC       (G(i/o/t/z)).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X04828; CAA28512.1; -.
DR   EMBL; X07854; CAA30703.1; -.
DR   EMBL; M20593; AAA35894.1; -.
DR   EMBL; M20586; AAA35894.1; JOINED.
DR   EMBL; M20587; AAA35894.1; JOINED.
DR   EMBL; M20588; AAA35894.1; JOINED.
DR   EMBL; M20589; AAA35894.1; JOINED.
DR   EMBL; M20590; AAA35894.1; JOINED.
DR   EMBL; M20591; AAA35894.1; JOINED.
DR   EMBL; M20592; AAA35894.1; JOINED.
DR   EMBL; AF493906; AAM12620.1; -.
DR   EMBL; BC012138; AAH12138.1; -.
DR   EMBL; J03004; AAA52556.1; ALT_SEQ.
DR   PIR; S02319; RGHUI2.
DR   HSSP; P10824; 1AS3.
DR   Genew; HGNC:4385; GNAI2.
DR   H-InvDB; HIX0003320; -.
DR   MIM; 139360; -.
DR   GO; GO:0003927; F:heterotrimeric G-protein GTPase activity; TAS.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
DR   GO; GO:0007194; P:negative regulation of adenylate cyclase ac. . .; TAS.
DR   GO; GO:0007584; P:response to nutrients; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR001019; Gprotein_alpha.
DR   InterPro; IPR001408; Gprotein_alphaI.
DR   InterPro; IPR011025; Transducn_insert.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   PRINTS; PR00441; GPROTEINAI.
DR   ProDom; PD000281; Gprotein_alpha; 1.
KW   ADP-ribosylation; GTP-binding; Lipoprotein; Multigene family;
KW   Myristate; Palmitate; Transducer.
FT   INIT_MET      0      0       By similarity.
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   LIPID         2      2       S-palmitoyl cysteine (By similarity).
FT   NP_BIND      39     46       GTP (By similarity).
FT   NP_BIND     200    204       GTP (By similarity).
FT   NP_BIND     269    272       GTP (By similarity).
FT   MOD_RES     178    178       ADP-ribosylarginine (by cholera toxin).
FT   MOD_RES     351    351       ADP-ribosylcysteine (by pertussis toxin).
SQ   SEQUENCE   354 AA;  40319 MW;  6E66B102DA0088EB CRC64;

  Query Match             100.0%;  Score 57;  DB 1;  Length 354;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        345 KNNLKDCGLF 354


RESULT 21
GBI2_MOUSE
ID   GBI2_MOUSE     STANDARD;      PRT;   354 AA.
AC   P08752;
DT   01-NOV-1988 (Rel. 09, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Guanine nucleotide-binding protein G(i), alpha-2 subunit (Adenylate
DE   cyclase-inhibiting G alpha protein).
GN   Name=Gnai2; Synonyms=Gnai-2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86313643; PubMed=3092218;
RA   Sullivan K.A., Liao Y.-C., Alborzi A., Beiderman B., Chang F.-H.,
RA   Masters S.B., Levinson A.D., Bourne H.R.;
RT   "Inhibitory and stimulatory G proteins of adenylate cyclase: cDNA and
RT   amino acid sequences of the alpha chains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 83:6687-6691(1986).
RN   [2]
RP   SEQUENCE OF 22-354 FROM N.A.
RX   MEDLINE=94224112; PubMed=8170357; DOI=10.1016/0169-328X(94)90267-4;
RA   Tachibana M., Asano T., Wilcox E., Yokotani N., Rivolta M.N., Fex J.;
RT   "G protein Gi2 alpha in the cochlea: cloning and selective occurrence
RT   in receptor cells.";
RL   Brain Res. Mol. Brain Res. 21:355-358(1994).
CC   -!- FUNCTION: Guanine nucleotide-binding proteins (G proteins) are
CC       involved as modulators or transducers in various transmembrane
CC       signaling systems. The G(i) proteins are involved in hormonal
CC       regulation of adenylate cyclase: they inhibit the cyclase in
CC       response to beta-adrenergic stimuli.
CC   -!- SUBUNIT: G proteins are composed of 3 units; alpha, beta and
CC       gamma. The alpha chain contains the guanine nucleotide binding
CC       site. Interacts with UNC5B (By similarity).
CC   -!- SIMILARITY: Belongs to the G-alpha family. Subfamily 1
CC       (G(i/o/t/z)).
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; M13963; AAA37692.1; -.
DR   EMBL; S71213; AAB30632.2; -.
DR   PIR; B25889; RGMSI2.
DR   HSSP; P10824; 1AS3.
DR   MGD; MGI:95772; Gnai2.
DR   GO; GO:0007213; P:acetyl choline receptor signaling, muscarin. . .; IMP.
DR   GO; GO:0007193; P:G-protein signaling, adenylate cyclase inhi. . .; IMP.
DR   InterPro; IPR001019; Gprotein_alpha.
DR   InterPro; IPR001408; Gprotein_alphaI.
DR   InterPro; IPR011025; Transducn_insert.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   PRINTS; PR00441; GPROTEINAI.
DR   ProDom; PD000281; Gprotein_alpha; 1.
KW   ADP-ribosylation; GTP-binding; Lipoprotein; Multigene family;
KW   Myristate; Palmitate; Transducer.
FT   INIT_MET      0      0       By similarity.
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   LIPID         2      2       S-palmitoyl cysteine (By similarity).
FT   NP_BIND      39     46       GTP (By similarity).
FT   NP_BIND     200    204       GTP (By similarity).
FT   NP_BIND     269    272       GTP (By similarity).
FT   MOD_RES     178    178       ADP-ribosylarginine (by cholera toxin).
FT   MOD_RES     351    351       ADP-ribosylcysteine (by pertussis toxin).
FT   CONFLICT     81     81       L -> I (in Ref. 2).
FT   CONFLICT     86     86       A -> R (in Ref. 1).
SQ   SEQUENCE   354 AA;  40339 MW;  40A7CA30EDDC3778 CRC64;

  Query Match             100.0%;  Score 57;  DB 1;  Length 354;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        345 KNNLKDCGLF 354


RESULT 22
GBI2_ORYLA
ID   GBI2_ORYLA     STANDARD;      PRT;   354 AA.
AC   O13055;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Guanine nucleotide-binding protein G(i), alpha-2 subunit (Adenylate
DE   cyclase-inhibiting G alpha protein) (Gi2 alpha subunit) (Gi alpha c).
GN   Name=GNAI2;
OS   Oryzias latipes (Medaka fish) (Japanese ricefish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC   Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
OX   NCBI_TaxID=8090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RX   MEDLINE=98055713; PubMed=9395335;
RA   Oba Y., Yoshikuni M., Tanaka M., Mita M., Nagahama Y.;
RT   "Inhibitory guanine-nucleotide-binding-regulatory protein alpha
RT   subunits in medaka (Oryzias latipes) oocytes -- cDNA cloning and
RT   decreased expression of proteins during oocyte maturation.";
RL   Eur. J. Biochem. 249:846-853(1997).
CC   -!- FUNCTION: Guanine nucleotide-binding proteins (G proteins) are
CC       involved as modulators or transducers in various transmembrane
CC       signaling systems. The G(i) proteins are involved in hormonal
CC       regulation of adenylate cyclase: they inhibit the cyclase in
CC       response to beta-adrenergic stimuli.
CC   -!- SUBUNIT: G proteins are composed of 3 units; alpha, beta and
CC       gamma. The alpha chain contains the guanine nucleotide binding
CC       site.
CC   -!- SIMILARITY: Belongs to the G-alpha family. Subfamily 1
CC       (G(i/o/t/z)).
CC   ---------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; AB001742; BAA20073.1; -.
DR   HSSP; P10824; 1GDD.
DR   InterPro; IPR001019; Gprotein_alpha.
DR   InterPro; IPR001408; Gprotein_alphaI.
DR   InterPro; IPR011025; Transducn_insert.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   PRINTS; PR00441; GPROTEINAI.
DR   ProDom; PD000281; Gprotein_alpha; 1.
DR   SMART; SM00275; G_alpha; 1.
KW   ADP-ribosylation; GTP-binding; Lipoprotein; Multigene family;
KW   Myristate; Palmitate; Transducer.
FT   INIT_MET      0      0       By similarity.
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   LIPID         2      2       S-palmitoyl cysteine (By similarity).
FT   NP_BIND      39     46       GTP (By similarity).
FT   NP_BIND     200    204       GTP (By similarity).
FT   NP_BIND     269    272       GTP (By similarity).
FT   MOD_RES     178    178       ADP-ribosylarginine (by cholera toxin)
FT                                (By similarity).
FT   MOD_RES     351    351       ADP-ribosylcysteine (by pertussis toxin)
FT                                (By similarity).
SQ   SEQUENCE   354 AA;  40861 MW;  C5D64B0970E3BDD3 CRC64;

  Query Match             100.0%;  Score 57;  DB 1;  Length 354;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        345 KNNLKDCGLF 354


RESULT 23
GBI2_RAT
ID   GBI2_RAT       STANDARD;      PRT;   354 AA.
AC   P04897;
DT   13-AUG-1987 (Rel. 05, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
DT   25-JAN-2005 (Rel. 46, Last annotation update)
DE   Guanine nucleotide-binding protein G(i), alpha-2 subunit (Adenylate
DE   cyclase-inhibiting G alpha protein).
GN   Name=Gnai2; Synonyms=Gnai-2;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86233317; PubMed=3086867;
RA   Itoh H., Kozasa T., Nagata S., Nakamura S., Katada T., Ui M., Iwai S.,
RA   Ohtsuka E., Kawasaki H., Suzuki K., Kaziro Y.;
RT   "Molecular cloning and sequence determination of cDNAs for alpha
RT   subunits of the guanine nucleotide-binding proteins Gs, Gi, and Go
RT   from rat brain.";
RL   Proc. Natl. Acad. Sci. U.S.A. 83:3776-3780(1986).
RN   [2]
RP   SEQUENCE FROM N.A.
```

```
RX   MEDLINE=88007678; PubMed=2820999;
RA   Jones D.T., Reed R.R.;
RT   "Molecular cloning of five GTP-binding protein cDNA species from rat
RT   olfactory neuroepithelium.";
RL   J. Biol. Chem. 262:14241-14249(1987).
RN   [3]
RP   SEQUENCE OF 11-125.
RX   PubMed=2159473;
RA   Linder M.E., Ewald D.A., Miller R.J., Gilman A.G.;
RT   "Purification and characterization of Go alpha and three types of Gi
RT   alpha after expression in Escherichia coli.";
RL   J. Biol. Chem. 265:8243-8251(1990).
CC   -!- FUNCTION: Guanine nucleotide-binding proteins (G proteins) are
CC       involved as modulators or transducers in various transmembrane
CC       signaling systems. The G(i) proteins are involved in hormonal
CC       regulation of adenylate cyclase: they inhibit the cyclase in
CC       response to beta-adrenergic stimuli.
CC   -!- SUBUNIT: G proteins are composed of 3 units; alpha, beta and
CC       gamma. The alpha chain contains the guanine nucleotide binding
CC       site. Interacts with UNC5B (By similarity).
CC   -!- SIMILARITY: Belongs to the G-alpha family. Subfamily 1
CC       (G(i/o/t/z)).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M12672; AAA41260.1; -.
DR   EMBL; M17528; AAA40824.1; -.
DR   PIR; D27423; RGRTI2.
DR   HSSP; P10824; 1AS3.
DR   RGD; 620243; Gnai2.
DR   InterPro; IPR001019; Gprotein_alpha.
DR   InterPro; IPR001408; Gprotein_alphaI.
DR   InterPro; IPR011025; Transducn_insert.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   PRINTS; PR00441; GPROTEINAI.
DR   ProDom; PD000281; Gprotein_alpha; 1.
KW   ADP-ribosylation; Direct protein sequencing; GTP-binding; Lipoprotein;
KW   Multigene family; Myristate; Palmitate; Transducer.
FT   INIT_MET      0      0       By similarity.
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   LIPID         2      2       S-palmitoyl cysteine (By similarity).
FT   NP_BIND      39     46       GTP (By similarity).
FT   NP_BIND     200    204       GTP (By similarity).
FT   NP_BIND     269    272       GTP (By similarity).
FT   MOD_RES     178    178       ADP-ribosylarginine (by cholera toxin).
FT   MOD_RES     351    351       ADP-ribosylcysteine (by pertussis toxin).
FT   VARIANT     165    166       SD -> PN (in tryptic peptides).
SQ   SEQUENCE   354 AA;  40367 MW;  436B75599113FC19 CRC64;

  Query Match             100.0%;  Score 57;  DB 1;  Length 354;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        345 KNNLKDCGLF 354


RESULT 24
GBI_HOMAM
ID   GBI_HOMAM      STANDARD;      PRT;   354 AA.
AC   P41776;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Guanine nucleotide-binding protein G(i), alpha subunit (Adenylate
DE   cyclase-inhibiting G alpha protein).
OS   Homarus americanus (American lobster).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC   Nephropoidea; Nephropidae; Homarus.
OX   NCBI_TaxID=6706;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Olfactory organ;
RX   MEDLINE=93061797; PubMed=1279345; DOI=10.1016/0169-328X(92)90183-C;
RA   McClintock T.S., Byrnes A.P., Lerner M.R.;
RT   "Molecular cloning of a G-protein alpha i subunit from the lobster
RT   olfactory organ.";
RL   Brain Res. Mol. Brain Res. 14:273-276(1992).
CC   -!- FUNCTION: Guanine nucleotide-binding proteins (G proteins) are
CC       involved as modulators or transducers in various transmembrane
CC       signaling systems.
CC   -!- SUBUNIT: G proteins are composed of 3 units; alpha, beta and
CC       gamma. The alpha chain contains the guanine nucleotide binding
CC       site.
CC   -!- SIMILARITY: Belongs to the G-alpha family. Subfamily 1
CC       (G(i/o/t/z)).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S47614; AAB24072.2; ALT_SEQ.
DR   PIR; A48976; A48976.
DR   HSSP; P10824; 1AS3.
DR   InterPro; IPR001019; Gprotein_alpha.
DR   InterPro; IPR001408; Gprotein_alphaI.
DR   InterPro; IPR011025; Transducn_insert.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   PRINTS; PR00441; GPROTEINAI.
DR   ProDom; PD000281; Gprotein_alpha; 1.
KW   ADP-ribosylation; GTP-binding; Lipoprotein; Multigene family;
KW   Myristate; Transducer.
FT   INIT_MET      0      0       By similarity.
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   NP_BIND      40     47       GTP (By similarity).
FT   NP_BIND     200    204       GTP (By similarity).
FT   NP_BIND     269    272       GTP (By similarity).
FT   MOD_RES     178    178       ADP-ribosylarginine (by cholera toxin)
FT                                (By similarity).
FT   MOD_RES     351    351       ADP-ribosylcysteine (by pertussis toxin)
FT                                (By similarity).
FT   CONFLICT    308    323       Missing (in Ref. 1; AAB24072).
SQ   SEQUENCE   354 AA;  40600 MW;  1A032BDCBF83896D CRC64;

  Query Match             100.0%;  Score 57;  DB 1;  Length 354;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        345 KNNLKDCGLF 354


RESULT 25
Q8TAN5
ID   Q8TAN5      PRELIMINARY;      PRT;   354 AA.
AC   Q8TAN5;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Guanine nucleotide binding protein (G protein), alpha inhibiting
DE   activity polypeptide 1.
```

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GN   Name=GNAI1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC026326; AAH26326.1; -.
DR   HSSP; P10824; 1AGR.
DR   GO; GO:0005525; F:GTP binding; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR001019; Gprotein_alpha.
DR   InterPro; IPR001408; Gprotein_alphaI.
DR   InterPro; IPR011025; Transducn_insert.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   PRINTS; PR00441; GPROTEINAI.
DR   ProDom; PD000281; Gprotein_alpha; 1.
DR   SMART; SM00275; G_alpha; 1.
SQ   SEQUENCE   354 AA;  40362 MW;  DF2831AAF6F79D5F CRC64;

  Query Match             100.0%;  Score 57;  DB 2;  Length 354;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        345 KNNLKDCGLF 354


RESULT 26
Q9UGA4
ID   Q9UGA4       PRELIMINARY;      PRT;   354 AA.
AC   Q9UGA4;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Hypothetical protein DKFZp564K1216.
GN   Name=DKFZp564K1216;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=21154917; PubMed=11230166; DOI=10.1101/gr.GR1547R;
RA   Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
RA   Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H.,
RA   Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
RA   Mewes H.W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,
RA   Wambutt R., Korn B., Klein M., Poustka A.;
RT   "Towards a Catalog of Human Genes and Proteins: Sequencing and
RT   Analysis of 500 Novel Complete Protein Coding Human cDNAs.";
RL   Genome Res. 11:422-435(2001).
DR   EMBL; AL049933; CAB43212.2; -.
DR   HSSP; P10824; 1GDD.
DR   GO; GO:0005525; F:GTP binding; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR001019; Gprotein_alpha.
DR   InterPro; IPR001408; Gprotein_alphaI.
DR   InterPro; IPR011025; Transducn_insert.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   PRINTS; PR00441; GPROTEINAI.
DR   ProDom; PD000281; Gprotein_alpha; 1.
DR   SMART; SM00275; G_alpha; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   354 AA;  40347 MW;  C64BCB428685D423 CRC64;

  Query Match             100.0%;  Score 57;  DB 2;  Length 354;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        345 KNNLKDCGLF 354


RESULT 27
Q8WP45
ID   Q8WP45       PRELIMINARY;      PRT;   354 AA.
AC   Q8WP45;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   G protein alpha subunit i class.
GN   Name=HrGi-2; Synonyms=HrGi-1;
OS   Halocynthia roretzi (Sea squirt).
OC   Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC   Stolidobranchia; Pyuridae; Halocynthia.
OX   NCBI_TaxID=7729;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Iwasa T., Kanehara K., Watari A., Ohkuma M., Tsuda M.;
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB047083; BAB79198.1; -.
DR   EMBL; AB047082; BAB79197.1; -.
DR   HSSP; P10824; 1AS3.
DR   GO; GO:0005525; F:GTP binding; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   PRINTS; PR00441; GPROTEINAI.
DR   SMART; SM00275; G_alpha; 1.
SQ   SEQUENCE   354 AA;  40498 MW;  FC99F52B34BE1837 CRC64;

  Query Match             100.0%;  Score 57;  DB 2;  Length 354;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        345 KNNLKDCGLF 354
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RESULT 28
Q8WSS1
ID   Q8WSS1      PRELIMINARY;      PRT;   354 AA.
AC   Q8WSS1;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   G protein alpha subunit Gi splicing variant CiGi1b.
GN   Name=CiGi1;
OS   Ciona intestinalis.
OC   Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC   Phlebobranchia; Cionidae; Ciona.
OX   NCBI_TaxID=7719;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Yoshida R., Kusakabe T., Kamatani M., Iwasa T., Tsuda M.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB066282; BAB83918.1; -.
DR   HSSP; P10824; 1AS3.
DR   GO; GO:0005525; F:GTP binding; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   PRINTS; PR00441; GPROTEINAI.
DR   SMART; SM00275; G_alpha; 1.
SQ   SEQUENCE   354 AA;  40402 MW;  65526E6F197F9FB1 CRC64;

  Query Match           100.0%;  Score 57;  DB 2;  Length 354;
  Best Local Similarity  100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        345 KNNLKDCGLF 354


RESULT 29
Q8WSS2
ID   Q8WSS2      PRELIMINARY;      PRT;   354 AA.
AC   Q8WSS2;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   G protein alpha subunit Gi splicing variant CiGi1a.
GN   Name=CiGi1;
OS   Ciona intestinalis.
OC   Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC   Phlebobranchia; Cionidae; Ciona.
OX   NCBI_TaxID=7719;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Yoshida R., Kusakabe T., Kamatani M., Iwasa T., Tsuda M.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB066281; BAB83917.1; -.
DR   HSSP; P10824; 1AS3.
DR   GO; GO:0005525; F:GTP binding; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   PRINTS; PR00441; GPROTEINAI.
DR   ProDom; PD000281; Gprotein_alpha; 1.
DR   SMART; SM00275; G_alpha; 1.
SQ   SEQUENCE   354 AA;  40391 MW;  D5BEBD748D6AE92F CRC64;

  Query Match           100.0%;  Score 57;  DB 2;  Length 354;
  Best Local Similarity  100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        345 KNNLKDCGLF 354


RESULT 30
Q6QM16
ID   Q6QM16      PRELIMINARY;      PRT;   354 AA.
AC   Q6QM16;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Guanine nucleotide-binding protein G(I) alpha subunit (EC
DE   3.6.5.1).
OS   Lytechinus variegatus (Sea urchin).
OC   Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC   Echinoidea; Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae;
OC   Lytechinus.
OX   NCBI_TaxID=7654;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RX   PubMed=15003628; DOI=10.1016/j.mod.2004.01.005;
RA   Voronina E., Wessel G.M.;
RT   "Regulatory contribution of heterotrimeric G-proteins to oocyte
RT   maturation in the sea urchin.";
RL   Mech. Dev. 121:247-259(2004).
DR   EMBL; AY534104; AAS38581.1; -.
DR   HSSP; P10824; 1AS3.
DR   GO; GO:0005525; F:GTP binding; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR001019; Gprotein_alpha.
DR   InterPro; IPR001408; Gprotein_alphaI.
DR   InterPro; IPR011025; Transducn_insert.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   PRINTS; PR00441; GPROTEINAI.
DR   ProDom; PD000281; Gprotein_alpha; 1.
DR   SMART; SM00275; G_alpha; 1.
KW   Hydrolase.
SQ   SEQUENCE   354 AA;  40291 MW;  F211598F662FB5EB CRC64;

  Query Match           100.0%;  Score 57;  DB 2;  Length 354;
  Best Local Similarity  100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        345 KNNLKDCGLF 354


RESULT 31
Q6QM17
ID   Q6QM17      PRELIMINARY;      PRT;   354 AA.
AC   Q6QM17;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Guanine nucleotide-binding protein G(I) alpha subunit (EC
DE   3.6.5.1).
OS   Strongylocentrotus purpuratus (Purple sea urchin).
OC   Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC   Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC   Strongylocentrotus.
OX   NCBI_TaxID=7668;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RX   PubMed=15003628; DOI=10.1016/j.mod.2004.01.005;
RA   Voronina E., Wessel G.M.;
RT   "Regulatory contribution of heterotrimeric G-proteins to oocyte
RT   maturation in the sea urchin.";
RL   Mech. Dev. 121:247-259(2004).
DR   EMBL; AY534103; AAS38580.1; -.
```

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DR   HSSP; P10824; 1AS3.
DR   GO; GO:0005525; F:GTP binding; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR001019; Gprotein_alpha.
DR   InterPro; IPR001408; Gprotein_alphaI.
DR   InterPro; IPR011025; Transducn_insert.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   PRINTS; PR00441; GPROTEINAI.
DR   ProDom; PD000281; Gprotein_alpha; 1.
DR   SMART; SM00275; G_alpha; 1.
KW   Hydrolase.
SQ   SEQUENCE   354 AA;  40291 MW;  F211598F662FB5EB CRC64;

  Query Match             100.0%;  Score 57;  DB 2;  Length 354;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        345 KNNLKDCGLF 354


RESULT 32
Q9NL94
ID   Q9NL94      PRELIMINARY;      PRT;   354 AA.
AC   Q9NL94;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   G protein alpha subunit i class.
GN   Name=OvGai;
OS   Octopus vulgaris (Octopus).
OC   Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC   Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
OX   NCBI_TaxID=6645;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye;
RA   Iwasa T., Yanai T., Nakagawa M., Kikkawa S., Obata S., Usukura J.,
RA   Tsuda M.;
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB025780; BAA93636.1; -.
DR   HSSP; P10824; 1GDD.
DR   GO; GO:0005525; F:GTP binding; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR001019; Gprotein_alpha.
DR   InterPro; IPR001408; Gprotein_alphaI.
DR   InterPro; IPR011025; Transducn_insert.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   PRINTS; PR00441; GPROTEINAI.
DR   ProDom; PD000281; Gprotein_alpha; 1.
DR   SMART; SM00275; G_alpha; 1.
SQ   SEQUENCE   354 AA;  40660 MW;  C3764529365FEA04 CRC64;

  Query Match             100.0%;  Score 57;  DB 2;  Length 354;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        345 KNNLKDCGLF 354


RESULT 33
Q7T3D3
ID   Q7T3D3      PRELIMINARY;      PRT;   354 AA.
AC   Q7T3D3;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Similar to guanine nucleotide binding protein, alpha inhibiting
DE   1.
GN   Name=gnai1;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   Director MGC Project;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC053164; AAH53164.1; -.
DR   HSSP; P10824; 1AS3.
DR   ZFIN; ZDB-GENE-040426-1310; gnai1.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR001019; Gprotein_alpha.
DR   InterPro; IPR011025; Transducn_insert.
DR   Pfam; PF00503; G-alpha; 1.
DR   ProDom; PD000281; Gprotein_alpha; 1.
DR   SMART; SM00275; G_alpha; 1.
SQ   SEQUENCE   354 AA;  40329 MW;  AF9B7A3F0E0DA01C CRC64;

  Query Match             100.0%;  Score 57;  DB 2;  Length 354;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        345 KNNLKDCGLF 354


RESULT 34
Q96C71
ID   Q96C71      PRELIMINARY;      PRT;   355 AA.
AC   Q96C71;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Guanine nucleotide binding protein (G protein), alpha inhibiting
DE   activity polypeptide 2 (GNAI2 protein).
GN   Name=GNAI2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   Strausberg R.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC014627; AAH14627.1; -.
DR   EMBL; CR456783; CAG33064.1; -.
DR   HSSP; P10824; 1AS3.
DR   GO; GO:0005525; F:GTP binding; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR001019; Gprotein_alpha.
DR   InterPro; IPR001408; Gprotein_alphaI.
DR   InterPro; IPR011025; Transducn_insert.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   PRINTS; PR00441; GPROTEINAI.
DR   ProDom; PD000281; Gprotein_alpha; 1.
DR   SMART; SM00275; G_alpha; 1.
SQ   SEQUENCE   355 AA;  40493 MW;  B1C3DBE224D5937C CRC64;

  Query Match             100.0%;  Score 57;  DB 2;  Length 355;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        346 KNNLKDCGLF 355


RESULT 35
Q6P1C0
ID   Q6P1C0      PRELIMINARY;      PRT;   355 AA.
AC   Q6P1C0;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Guanine nucleotide binding protein, alpha inhibiting 2.
GN   Name=Gnai2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC065159; AAH65159.1; -.
DR   HSSP; P10824; 1AS3.
DR   GO; GO:0003924; F:GTPase activity; TAS.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0007213; P:acetylcholine receptor signaling, muscarini. . .; IMP.
DR   GO; GO:0007193; P:G-protein signaling, adenylate cyclase inhi. . .; IMP.
DR   GO; GO:0008016; P:regulation of heart rate; IMP.
DR   InterPro; IPR001019; Gprotein_alpha.
DR   InterPro; IPR001408; Gprotein_alphaI.
DR   InterPro; IPR011025; Transducn_insert.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   PRINTS; PR00441; GPROTEINAI.
DR   ProDom; PD000281; Gprotein_alpha; 1.
DR   SMART; SM00275; G_alpha; 1.
SQ   SEQUENCE   355 AA;  40489 MW;  90AC64AFA713493E CRC64;

  Query Match             100.0%;  Score 57;  DB 2;  Length 355;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        346 KNNLKDCGLF 355


RESULT 36
Q6P3M7
ID   Q6P3M7      PRELIMINARY;      PRT;   355 AA.
AC   Q6P3M7;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein MGC76300.
GN   Name=MGC76300;
OS   Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8364;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RA   Klein S., Gerhard D.S.;
RL   Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC063931; AAH63931.1; -.
DR   HSSP; P10824; 1AS3.
DR   GO; GO:0005525; F:GTP binding; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR001019; Gprotein_alpha.
DR   InterPro; IPR001408; Gprotein_alphaI.
DR   InterPro; IPR011025; Transducn_insert.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   PRINTS; PR00441; GPROTEINAI.
DR   ProDom; PD000281; Gprotein_alpha; 1.
DR   SMART; SM00275; G_alpha; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   355 AA;  40434 MW;  444F15DA90FCE6C6 CRC64;

  Query Match             100.0%;  Score 57;  DB 2;  Length 355;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        346 KNNLKDCGLF 355


RESULT 37
Q6TNT8
ID   Q6TNT8      PRELIMINARY;      PRT;   355 AA.
AC   Q6TNT8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Guanine nucleotide binding protein (G protein), alpha inhibiting
DE   activity polypeptide 2 (Similar to guanine nucleotide binding protein,
DE   alpha inhibiting 2).
GN   Name=gnai2l; Synonyms=GNAI2;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Song H.D., Wu X.Y., Sun X.J., Zhou Y., Liu T.X., Deng M., Zhang G.W.,
RA   Sheng Y., Chen Y., Ruan Z., Jiang C.L., Fan H.Y., Zon L.I.,
RA   KanKi J.P., Look A.T., Chen Z.;
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Director MGC Project;
RL   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY391429; AAQ91241.1; -.
DR   EMBL; BC076100; AAH76100.1; -.
DR   HSSP; P10824; 1AS3.
DR   ZFIN; ZDB-GENE-030131-8365; gnai2l.
DR   GO; GO:0005525; F:GTP binding; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR001019; Gprotein_alpha.
DR   InterPro; IPR001408; Gprotein_alphaI.
DR   InterPro; IPR011025; Transducn_insert.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   PRINTS; PR00441; GPROTEINAI.
DR   ProDom; PD000281; Gprotein_alpha; 1.
DR   SMART; SM00275; G_alpha; 1.
SQ   SEQUENCE   355 AA;  40836 MW;  F14AE52E7DEBA61E CRC64;

  Query Match             100.0%;  Score 57;  DB 2;  Length 355;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        346 KNNLKDCGLF 355


RESULT 38
Q9W6A4
ID   Q9W6A4      PRELIMINARY;      PRT;   355 AA.
AC   Q9W6A4;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Guanine nucleotide-binding protein Gi2 alpha-subunit.
OS   Squalus acanthias (Spiny dogfish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC   Elasmobranchii; Squalea; Hypnosqualea; Squaliformes; Squaloidei;
OC   Squalidae; Squalus.
OX   NCBI_TaxID=7797;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Rectal gland;
RA   George A.A., Aller S.G., Forrest J.N. Jr.;
RT   "Cloning of Multiple G-protein Alpha Subunits and Characterization of
RT   a Full Length Gi-alpha-2 from the Shark (Squalus acanthias) Rectal
RT   Gland.";
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RL   Bull. Mt. Desert Isl. Biol. Lab. 37:60-63(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Rectal gland;
RA   George A.A., Aller S.G., Forrest J.N. Jr.;
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF109173; AAD26121.2; -.
DR   HSSP; P10824; 1AS3.
DR   GO; GO:0005525; F:GTP binding; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR001019; Gprotein_alpha.
DR   InterPro; IPR001408; Gprotein_alphaI.
DR   InterPro; IPR011025; Transducn_insert.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   PRINTS; PR00441; GPROTEINAI.
DR   ProDom; PD000281; Gprotein_alpha; 1.
DR   SMART; SM00275; G_alpha; 1.
SQ   SEQUENCE   355 AA;  40285 MW;  A3ACD0314E81763A CRC64;

  Query Match           100.0%;  Score 57;  DB 2;  Length 355;
  Best Local Similarity  100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        346 KNNLKDCGLF 355


RESULT 39
Q7Q6E0
ID   Q7Q6E0      PRELIMINARY;      PRT;   357 AA.
AC   Q7Q6E0;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   AgCP5651 (Fragment).
GN   Name=agCG54259; ORFNames=ENSANGG00000011071;
OS   Anopheles gambiae str. PEST.
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX   NCBI_TaxID=180454;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=PEST;
RA   Anopheles Genome Sequencing Consortium;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAAB01008960; EAA11917.1; -.
DR   HSSP; P10824; 1AS3.
DR   GO; GO:0005525; F:GTP binding; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR001019; Gprotein_alpha.
DR   InterPro; IPR001408; Gprotein_alphaI.
DR   InterPro; IPR011025; Transducn_insert.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   PRINTS; PR00441; GPROTEINAI.
DR   ProDom; PD000281; Gprotein_alpha; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   357 AA;  40876 MW;  A1295839894509A7 CRC64;

  Query Match           100.0%;  Score 57;  DB 2;  Length 357;
  Best Local Similarity  100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        348 KNNLKDCGLF 357


RESULT 40
Q7ZW82
ID   Q7ZW82      PRELIMINARY;      PRT;   377 AA.
AC   Q7ZW82;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Guanine nucleotide binding protein (G protein), alpha inhibiting
DE   activity polypeptide a.
GN   Name=gnaia;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Whole body;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Whole body;
RA   Strausberg R.;
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC049537; AAH49537.1; -.
DR   HSSP; P10824; 1GDD.
DR   ZFIN; ZDB-GENE-030131-2229; gnaia.
DR   GO; GO:0005525; F:GTP binding; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR001019; Gprotein_alpha.
DR   InterPro; IPR001408; Gprotein_alphaI.
DR   InterPro; IPR011025; Transducn_insert.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   PRINTS; PR00441; GPROTEINAI.
DR   ProDom; PD000281; Gprotein_alpha; 1.
DR   SMART; SM00275; G_alpha; 1.
SQ   SEQUENCE   377 AA;  43655 MW;  2E3C56595403E00D CRC64;

  Query Match           100.0%;  Score 57;  DB 2;  Length 377;
  Best Local Similarity  100.0%;  Pred. No. 0.03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        368 KNNLKDCGLF 377


Search completed: March 22, 2005, 06:40:55
Job time : 58 secs
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OM protein - protein search, using sw model

Run on: March 22, 2005, 06:00:26 ; Search time 15 Seconds
(without alignments)
64.145 Million cell updates/sec

Title: US-10-009-809-2
Perfect score: 57
Sequence: 1 KNNLKDCGLF 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	57	100.0	354	1	RGBOI1	GTP-binding regula
2	57	100.0	354	1	RGHUI1	GTP-binding regula
3	57	100.0	354	1	RGRTI1	GTP-binding regula
4	57	100.0	354	1	RGXLI1	GTP-binding regula
5	57	100.0	354	2	S28157	GTP-binding regula
6	57	100.0	354	2	S24362	GTP-binding regula
7	57	100.0	354	2	I50237	GTP-binding regula
8	57	100.0	354	2	S27013	GTP-binding regula
9	57	100.0	355	1	RGHUI2	GTP-binding regula
10	57	100.0	355	1	RGMSI2	GTP-binding regula
11	57	100.0	355	1	RGRTI2	GTP-binding regula
12	57	100.0	355	2	S28158	GTP-binding regula
13	57	100.0	355	2	I50238	Gi2 protein alpha-
14	57	100.0	355	2	A61031	GTP-binding regula
15	57	100.0	355	2	A48976	GTP-binding regula
16	51	89.5	350	1	RGBOT1	GTP-binding regula
17	51	89.5	350	1	RGHUT1	GTP-binding regula
18	51	89.5	350	1	RGMST1	GTP-binding regula
19	51	89.5	354	1	RGBOT2	GTP-binding regula
20	51	89.5	354	1	RGHUT2	GTP-binding regula
21	51	89.5	354	2	S24352	gustducin - rat
22	50	87.7	63	2	I48071	GTP binding protei
23	50	87.7	354	1	RGHUI3	GTP-binding regula
24	50	87.7	354	1	RGRTI3	GTP-binding regula
25	50	87.7	354	2	S28159	GTP-binding regula
26	50	87.7	354	2	S40508	GTP-binding regula
27	50	87.7	354	2	S40509	G-protein - chicke
28	49	86.0	104	2	B25888	probable GTP-bindi
29	41	71.9	355	1	RGFFA	GTP-binding regula
30	40	70.2	394	2	B69619	phosphodeoxyribomu
31	39	68.4	345	1	RGXLI3	GTP-binding regula
32	39	68.4	354	1	RGHYO1	GTP-binding regula
33	39	68.4	354	1	RGBOO1	GTP-binding regula
34	39	68.4	354	1	RGFFO1	GTP-binding regula
35	39	68.4	354	1	RGFFO2	GTP-binding regula
36	39	68.4	354	1	RGHUO1	GTP-binding regula
37	39	68.4	354	1	RGMSO1	GTP-binding regula
38	39	68.4	354	1	RGRTO1	GTP-binding regula
39	39	68.4	354	2	T19476	hypothetical prote
40	39	68.4	354	2	S27014	GTP-binding regula
41	39	68.4	354	2	A61035	GTP-binding regula
42	39	68.4	472	1	T10889	1-aminocyclopropan
43	39	68.4	778	2	C71944	hypothetical prote
44	38	66.7	480	2	T26614	hypothetical prote
45	38	66.7	1240	2	T48800	SMT4 related prote

ALIGNMENTS

RESULT 1
RGBOI1
GTP-binding regulatory protein Gi alpha-1 chain (adenylate cyclase-inhibiting) - bovine
N;Alternate names: guanine nucleotide binding protein Gi alpha-1 chain; heterotrimeric
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: A23631; A25888
R;Nukada, T.; Tanabe, T.; Takahashi, H.; Noda, M.; Haga, K.; Haga, T.; Ichiyama, A.; Ka
FEBS Lett. 197, 305-310, 1986
A;Title: Primary structure of the alpha-subunit of bovine adenylate cyclase-inhibiting
A;Reference number: A23631; MUID:86136587; PMID:2419165
A;Accession: A23631
A;Molecule type: mRNA
A;Residues: 1-354 <NUK>
A;Cross-references: UNIPROT:P04898; GB:X03642; NID:g390; PIDN:CAA27288.1; PID:g391
R;Michel, T.; Winslow, J.W.; Smith, J.A.; Seidman, J.G.; Neer, E.J.
Proc. Natl. Acad. Sci. U.S.A. 83, 7663-7667, 1986
A;Title: Molecular cloning and characterization of cDNA encoding the GTP-binding protei
A;Reference number: A94131; MUID:87017009; PMID:3094012
A;Accession: A25888
A;Molecule type: mRNA
A;Residues: 106-112,'S',114-329,'N',331-336,'E',338-354 <MIC>
A;Cross-references: GB:M14207; NID:g163129; PIDN:AAA30561.1; PID:g163130
C;Comment: The G proteins are a family of guanine nucleotide-binding proteins that rela
ains. The beta and gamma chains, required for GTPase activity, appear to be common to a
rase; it is specific for each type of G protein.
C;Comment: The Gi alpha chain is specific for G protein that is involved in hormonal re
C;Superfamily: GTP-binding regulatory protein Gs alpha chain
C;Keywords: blocked amino end; GTP binding; heterotrimer; lipoprotein; myristylation; n
F;2-354/Product: GTP-binding regulatory protein Gi alpha-1 chain #status predicted <MAT
F;40-47/Region: nucleotide-binding motif A (P-loop)
F;269-272/Region: GTP-binding NKXD motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3/Binding site: palmitate (Cys) (covalent) #status predicted
F;178/Modified site: ADP-ribosylarginine (Arg) (by cholera toxin) #status predicted
F;351/Modified site: ADP-ribosylcysteine (Cys) (by pertussis toxin) #status predicted

Query Match 100.0%; Score 57; DB 1; Length 354;
Best Local Similarity 100.0%; Pred. No. 0.0094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 345 KNNLKDCGLF 354

RESULT 2
RGHUI1
GTP-binding regulatory protein Gi alpha-1 chain (adenylate cyclase-inhibiting) - human
N;Alternate names: guanine nucleotide binding protein Gi alpha-1 chain; heterotrimeric
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004

C;Accession: A28318; D28154; T08669
R;Bray, P.; Carter, A.; Guo, V.; Puckett, C.; Kamholz, J.; Spiegel, A.; Nirenberg, M.
Proc. Natl. Acad. Sci. U.S.A. 84, 5115-5119, 1987
A;Title: Human cDNA clones for an alpha subunit of Gi signal-transduction protein.
A;Reference number: A28318; MUID:87260939; PMID:3110783
A;Accession: A28318
A;Molecule type: mRNA
A;Residues: 6-354 <BRA>
A;Cross-references: UNIPROT:P04898; GB:M17219; NID:g183410; PIDN:AAA52581.1; PID:g386747
R;Itoh, H.; Toyama, R.; Kozasa, T.; Tsukamoto, T.; Matsuoka, M.; Kaziro, Y.
J. Biol. Chem. 263, 6656-6664, 1988
A;Title: Presence of three distinct molecular species of G-i protein alpha-subunit. Stru
A;Reference number: A28154; MUID:88198230; PMID:2834384
A;Accession: D28154
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-101 <ITO>
A;Cross-references: GB:M20596; GB:M19476; NID:g183189; PIDN:AAA35893.1; PID:g183191
R;Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, March 1999
A;Reference number: Z16467
A;Accession: T08669
A;Molecule type: mRNA
A;Residues: 'WGGCSAATGGSAAATVPRDSKPQTRDLGALSRAGKQSLVVRNSRPLLSAPLRTASPSTPLRKWWGRRGPRREAFE
A;Cross-references: EMBL:AL049933
A;Experimental source: fetal brain; clone DKFZp564K1216
A;Note: differences are due to different assignment of start codons
C;Comment: The G proteins are a family of guanine nucleotide-binding proteins that relay
ains. The beta and gamma chains, required for GTPase activity, appear to be common to al
rase; it is specific for each type of G protein.
C;Comment: The Gi alpha chain is specific for G protein that is involved in hormonal reg
C;Genetics:
A;Gene: GDB:GNAI1
A;Cross-references: GDB:120001; OMIM:139310
A;Map position: 7q21-7q21
A;Note: DKFZp564K1216.1
C;Superfamily: GTP-binding regulatory protein Gs alpha chain
C;Keywords: blocked amino end; GTP binding; heterotrimer; lipoprotein; myristylation; nu
F;2-354/Product: GTP-binding regulatory protein Gi alpha-1 chain #status predicted <MAT>
F;40-47/Region: nucleotide-binding motif A (P-loop)
F;269-272/Region: GTP-binding NKXD motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3/Binding site: palmitate (Cys) (covalent) #status predicted
F;178/Modified site: ADP-ribosylarginine (Arg) (by cholera toxin) #status predicted
F;351/Modified site: ADP-ribosylcysteine (Cys) (by pertussis toxin) #status predicted

Query Match 100.0%; Score 57; DB 1; Length 354;
Best Local Similarity 100.0%; Pred. No. 0.0094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 345 KNNLKDCGLF 354

RESULT 3
RGRTI1
GTP-binding regulatory protein Gi alpha-1 chain (adenylate cyclase-inhibiting) - rat
N;Alternate names: guanine nucleotide binding protein Gi alpha-1 chain; heterotrimeric G
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: C27423
R;Jones, D.T.; Reed, R.R.
J. Biol. Chem. 262, 14241-14249, 1987
A;Title: Molecular cloning of five GTP-binding protein cDNA species from rat olfactory n
A;Reference number: A92614; MUID:88007678; PMID:2820999
A;Accession: C27423
A;Molecule type: mRNA
A;Residues: 1-354 <JON>
A;Cross-references: UNIPROT:P10824; GB:M17527; NID:g203167; PIDN:AAA40825.1; PID:g203168
C;Comment: The G proteins are a family of guanine nucleotide-binding proteins that relay
ains. The beta and gamma chains, required for GTPase activity, appear to be common to al
rase; it is specific for each type of G protein.
C;Comment: The Gi alpha chain is specific for G protein that is involved in hormonal re
C;Superfamily: GTP-binding regulatory protein Gs alpha chain
C;Keywords: blocked amino end; GTP binding; heterotrimer; lipoprotein; myristylation; nu
F;2-354/Product: GTP-binding regulatory protein Gi alpha-1 chain #status predicted <MAT:
F;40-47/Region: nucleotide-binding motif A (P-loop)
F;269-272/Region: GTP-binding NKXD motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3/Binding site: palmitate (Cys) (covalent) #status predicted
F;178/Modified site: ADP-ribosylarginine (Arg) (by cholera toxin) #status predicted
F;351/Modified site: ADP-ribosylcysteine (Cys) (by pertussis toxin) #status predicted

Query Match 100.0%; Score 57; DB 1; Length 354;
Best Local Similarity 100.0%; Pred. No. 0.0094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 345 KNNLKDCGLF 354

RESULT 4
RGXLI1
GTP-binding regulatory protein Gi alpha-1 chain (adenylate cyclase-inhibiting) - Africa
N;Alternate names: guanine nucleotide binding protein Gi alpha-1 chain; heterotrimeric
C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: S11045
R;Olate, J.; Martinez, S.; Purcell, P.; Jorquera, H.; Codina, J.; Birnbaumer, L.; Allen
FEBS Lett. 268, 27-31, 1990
A;Title: Molecular cloning and sequence determination of four different cDNA species co
A;Reference number: S11045; MUID:90346157; PMID:2116977
A;Accession: S11045
A;Molecule type: mRNA
A;Residues: 1-354 <OLA>
A;Cross-references: UNIPROT:P27044; GB:X56089; NID:g64707; PIDN:CAA39569.1; PID:g64708
C;Comment: The G proteins are a family of guanine nucleotide-binding proteins that relay
ains. The beta and gamma chains, required for GTPase activity, appear to be common to al
rase; it is specific for each type of G protein.
C;Comment: The Gi alpha chain is specific for G protein that is involved in hormonal re
C;Superfamily: GTP-binding regulatory protein Gs alpha chain
C;Keywords: blocked amino end; GTP binding; heterotrimer; lipoprotein; myristylation; nu
F;2-354/Product: GTP-binding regulatory protein Gi alpha-1 chain #status predicted <MAT
F;40-47/Region: nucleotide-binding motif A (P-loop)
F;269-272/Region: GTP-binding NKXD motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3/Binding site: palmitate (Cys) (covalent) #status predicted
F;178/Modified site: ADP-ribosylarginine (Arg) (by cholera toxin) #status predicted
F;351/Modified site: ADP-ribosylcysteine (Cys) (by pertussis toxin) #status predicted

Query Match 100.0%; Score 57; DB 1; Length 354;
Best Local Similarity 100.0%; Pred. No. 0.0094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 345 KNNLKDCGLF 354

RESULT 5
S28157
GTP-binding regulatory protein Gi alpha-1 chain - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 02-Feb-2001
C;Accession: S28157
R;Sakanaka, C.; Izumi, T.; Nakamura, M.; Honda, Z.; Watanabe, T.; Minami, M.; Mutoh, H.
Biochim. Biophys. Acta 1175, 61-66, 1992
A;Title: Three types of Gialpha protein of the guinea-pig lung: cDNA cloning and analys
A;Reference number: S28157; MUID:93129640; PMID:1482697
A;Accession: S28157
A;Molecule type: mRNA
A;Residues: 1-354 <SAK>
C;Superfamily: GTP-binding regulatory protein Gs alpha chain
C;Keywords: blocked amino end; GTP binding; lipoprotein; myristylation; nucleotide bind

F;40-47/Region: nucleotide-binding motif A (P-loop)
F;269-272/Region: GTP-binding NKXD motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3/Binding site: palmitate (Cys) (covalent) #status predicted
F;178/Modified site: ADP-ribosylarginine (Arg) (by cholera toxin) #status predicted

Query Match 100.0%; Score 57; DB 2; Length 354;
Best Local Similarity 100.0%; Pred. No. 0.0094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        345 KNNLKDCGLF 354
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RESULT 6
S24362
GTP-binding regulatory protein alpha chain - starfish (Asterina pectinifera)
C;Species: Asterina pectinifera
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S24362
R;Chiba, K.; Tadenuma, H.; Matsumoto, M.; Takahashi, K.; Katada, T.; Hoshi, M.
Eur. J. Biochem. 207, 833-838, 1992
A;Title: The primary structure of the alpha subunit of a starfish guanosine-nucleotide-b
A;Reference number: S24362; MUID:92362619; PMID:1499560
A;Accession: S24362
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-354 <CHI>
A;Cross-references: UNIPROT:P30676; EMBL:X66378; NID:g5646; PIDN:CAA47019.1; PID:g5647
C;Superfamily: GTP-binding regulatory protein Gs alpha chain
C;Keywords: GTP binding; nucleotide binding; P-loop
F;40-47/Region: nucleotide-binding motif A (P-loop)
F;269-272/Region: GTP-binding NKXD motif

Query Match 100.0%; Score 57; DB 2; Length 354;
Best Local Similarity 100.0%; Pred. No. 0.0094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        345 KNNLKDCGLF 354
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RESULT 7
I50237
GTP-binding regulatory protein Gi alpha-1 chain - chicken
N;Alternate names: Gi1 protein alpha chain
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50237
R;Kilbourne, E.J.; Galper, J.B.
Gene 150, 341-344, 1994
A;Title: Cloning of cDNAs coding for the G alpha i1 and G alpha i2 G-proteins from chick
A;Reference number: I50237; MUID:95121926; PMID:7821803
A;Accession: I50237
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-354 <KIL>
A;Cross-references: UNIPROT:P50146; GB:L24548; NID:g666870; PIDN:AAA65066.1; PID:g666871
C;Superfamily: GTP-binding regulatory protein Gs alpha chain
C;Keywords: blocked amino end; GTP binding; lipoprotein; myristylation; nucleotide bindi
F;40-47/Region: nucleotide-binding motif A (P-loop)
F;269-272/Region: GTP-binding NKXD motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3/Binding site: palmitate (Cys) (covalent) #status predicted
F;178/Modified site: ADP-ribosylarginine (Arg) (by cholera toxin) #status predicted

Query Match 100.0%; Score 57; DB 2; Length 354;
Best Local Similarity 100.0%; Pred. No. 0.0094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        345 KNNLKDCGLF 354
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RESULT 8
S27013
GTP-binding regulatory protein Gi alpha chain - great pond snail
N;Alternate names: guanine nucleotide-binding protein Gi alpha-1 chain
C;Species: Lymnaea stagnalis (great pond snail)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C;Accession: S27013; S25588
R;Knol, J.C.; Weidemann, W.; Planta, R.J.; Vreugdenhil, E.; van Heerikhuizen, H.
FEBS Lett. 314, 215-219, 1992
A;Title: Molecular cloning of G protein alpha subunits from the central nervous system
A;Reference number: S27013; MUID:93106153; PMID:1468550
A;Accession: S27013
A;Molecule type: mRNA
A;Residues: 1-354 <KNO>
A;Cross-references: UNIPROT:P30682; EMBL:Z15095; NID:g9630; PIDN:CAA78807.1; PID:g9631
C;Superfamily: GTP-binding regulatory protein Gs alpha chain
C;Keywords: GTP binding; heterotrimer; nucleotide binding; P-loop; signal transduction
F;40-47/Region: nucleotide-binding motif A (P-loop)
F;269-272/Region: GTP-binding NKXD motif

Query Match 100.0%; Score 57; DB 2; Length 354;
Best Local Similarity 100.0%; Pred. No. 0.0094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        345 KNNLKDCGLF 354
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RESULT 9
RGHUI2
GTP-binding regulatory protein Gi alpha-2 chain (adenylate cyclase-inhibiting) - human
N;Alternate names: guanine nucleotide binding protein Gi alpha-2 chain; heterotrimeric
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: S02319; A29025; B28154; S00618; S02320
R;Beals, C.R.; Wilson, C.B.; Perlmutter, R.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 7886-7890, 1987
A;Title: A small multigene family encodes G(i) signal-transduction proteins.
A;Reference number: S02319; MUID:88068503; PMID:3120178
A;Accession: S02319
A;Molecule type: mRNA
A;Residues: 1-355 <BEA>
A;Cross-references: UNIPROT:P04899; EMBL:J03004; NID:g183181; PIDN:AAA52556.1; PID:g183
R;Didsbury, J.R.; Ho, Y.S.; Snyderman, R.
FEBS Lett. 211, 160-164, 1987
A;Title: Human Gi protein alpha-subunit: deduction of amino acid structure from a clone
A;Reference number: A29025; MUID:87105966; PMID:3100330
A;Accession: A29025
A;Molecule type: mRNA
A;Residues: 1-355 <DID>
A;Cross-references: EMBL:X04828; NID:g31743; PIDN:CAA28512.1; PID:g31744
R;Itoh, H.; Toyama, R.; Kozasa, T.; Tsukamoto, T.; Matsuoka, M.; Kaziro, Y.
J. Biol. Chem. 263, 6656-6664, 1988
A;Title: Presence of three distinct molecular species of G-i protein alpha-subunit. Str
A;Reference number: A28154; MUID:88198230; PMID:2834384
A;Accession: B28154
A;Molecule type: mRNA
A;Residues: 1-355 <ITO>
A;Cross-references: GB:J03221
R;Weinstein, L.S.; Spiegel, A.M.; Carter, A.D.
FEBS Lett. 232, 333-340, 1988
A;Title: Cloning and characterization of the human gene for the alpha-subunit of Gi2, a
A;Reference number: S00618; MUID:88242822; PMID:2837412
A;Accession: S00618
A;Molecule type: DNA
A;Residues: 1-39 <WEI>
A;Cross-references: EMBL:X07854; NID:g31739; PIDN:CAA30703.1; PID:g31740
C;Comment: The G proteins are a family of guanine nucleotide-binding proteins that rela

ains. The beta and gamma chains, required for GTPase activity, appear to be common to al
rase; it is specific for each type of G protein.
C;Comment: The Gi alpha chain is specific for G protein that is involved in hormonal reg
C;Genetics:
A;Gene: GDB:GNAI2; GNAI2B
A;Cross-references: GDB:120516; OMIM:139360
A;Map position: 3p21.3-3p21.2
A;Introns: 40/1; 54/2; 101/3; 155/2; 198/2; 241/3; 293/1
C;Superfamily: GTP-binding regulatory protein Gs alpha chain
C;Keywords: blocked amino end; GTP binding; heterotrimer; lipoprotein; myristylation; nu
F;2-355/Product: GTP-binding regulatory protein Gi alpha-2 chain #status predicted <MAT>
F;40-47/Region: nucleotide-binding motif A (P-loop)
F;270-273/Region: GTP-binding NKXD motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3/Binding site: palmitate (Cys) (covalent) #status predicted
F;179/Modified site: ADP-ribosylarginine (Arg) (by cholera toxin) #status predicted
F;352/Modified site: ADP-ribosylcysteine (Cys) (by pertussis toxin) #status predicted

  Query Match 100.0%; Score 57; DB 1; Length 355;
  Best Local Similarity 100.0%; Pred. No. 0.0094;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
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Db 346 KNNLKDCGLF 355

RESULT 10
RGMSI2
GTP-binding regulatory protein Gi alpha-2 chain (adenylate cyclase-inhibiting) - mouse
N;Alternate names: guanine nucleotide binding protein Gi alpha-2 chain; heterotrimeric G
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: B25889
R;Sullivan, K.A.; Liao, Y.C.; Alborzi, A.; Beiderman, B.; Chang, F.H.; Masters, S.B.; Le
Proc. Natl. Acad. Sci. U.S.A. 83, 6687-6691, 1986
A;Title: Inhibitory and stimulatory G proteins of adenylate cyclase: cDNA and amino acid
A;Reference number: A94123; MUID:86313643; PMID:3092218
A;Accession: B25889
A;Molecule type: mRNA
A;Residues: 1-355 <SUL>
A;Cross-references: UNIPROT:P08752; GB:M13963; NID:g193513; PIDN:AAA37692.1; PID:g309255
C;Comment: The G proteins are a family of guanine nucleotide-binding proteins that relay
ains. The beta and gamma chains, required for GTPase activity, appear to be common to al
rase; it is specific for each type of G protein.
C;Comment: The Gi alpha chain is specific for G protein that is involved in hormonal reg
C;Superfamily: GTP-binding regulatory protein Gs alpha chain
C;Keywords: blocked amino end; GTP binding; heterotrimer; lipoprotein; myristylation; nu
F;2-355/Product: GTP-binding regulatory protein Gi alpha-2 chain #status predicted <MAT>
F;40-47/Region: nucleotide-binding motif A (P-loop)
F;270-273/Region: GTP-binding NKXD motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3/Binding site: palmitate (Cys) (covalent) #status predicted
F;179/Modified site: ADP-ribosylarginine (Arg) (by cholera toxin) #status predicted
F;352/Modified site: ADP-ribosylcysteine (Cys) (by pertussis toxin) #status predicted

  Query Match 100.0%; Score 57; DB 1; Length 355;
  Best Local Similarity 100.0%; Pred. No. 0.0094;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 346 KNNLKDCGLF 355

RESULT 11
RGRTI2
GTP-binding regulatory protein Gi alpha-2 chain (adenylate cyclase-inhibiting) - rat
N;Alternate names: guanine nucleotide binding protein Gi alpha-2 chain; heterotrimeric G
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: D27423; B24882; B35377
R;Jones, D.T.; Reed, R.R.
J. Biol. Chem. 262, 14241-14249, 1987
A;Title: Molecular cloning of five GTP-binding protein cDNA species from rat olfactory
A;Reference number: A92614; MUID:88007678; PMID:2820999
A;Accession: D27423
A;Molecule type: mRNA
A;Residues: 1-355 <JON>
A;Cross-references: UNIPROT:P04897; GB:M17528; NID:g203165; PIDN:AAA40824.1; PID:g20316
R;Itoh, H.; Kozasa, T.; Nagata, S.; Nakamura, S.; Katada, T.; Ui, M.; Iwai, S.; Ohtsuka,
Proc. Natl. Acad. Sci. U.S.A. 83, 3776-3780, 1986
A;Title: Molecular cloning and sequence determination of cDNAs for alpha subunits of the
A;Reference number: A94707; MUID:86233317; PMID:3086867
A;Accession: B24882
A;Molecule type: mRNA
A;Residues: 1-355 <ITO>
A;Cross-references: GB:M12672; NID:g204439; PIDN:AAA41260.1; PID:g204440
R;Linder, M.E.; Ewald, D.A.; Miller, R.J.; Gilman, A.G.
J. Biol. Chem. 265, 8243-8251, 1990
A;Title: Purification and characterization of G-oalpha and three types of G-ialpha after
A;Reference number: A35377; MUID:90243707; PMID:2159473
A;Accession: B35377
A;Molecule type: protein
A;Residues: 112-126 <LIN>
C;Comment: The G proteins are a family of guanine nucleotide-binding proteins that relay
ains. The beta and gamma chains, required for GTPase activity, appear to be common to al
rase; it is specific for each type of G protein.
C;Comment: The Gi alpha chain is specific for G protein that is involved in hormonal re
C;Superfamily: GTP-binding regulatory protein Gs alpha chain
C;Keywords: blocked amino end; GTP binding; heterotrimer; lipoprotein; myristylation; nu
F;2-355/Product: GTP-binding regulatory protein Gi alpha-2 chain #status predicted <MAT>
F;40-47/Region: nucleotide-binding motif A (P-loop)
F;270-273/Region: GTP-binding NKXD motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3/Binding site: palmitate (Cys) (covalent) #status predicted
F;179/Modified site: ADP-ribosylarginine (Arg) (by cholera toxin) #status predicted
F;352/Modified site: ADP-ribosylcysteine (Cys) (by pertussis toxin) #status predicted

  Query Match 100.0%; Score 57; DB 1; Length 355;
  Best Local Similarity 100.0%; Pred. No. 0.0094;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
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Db 346 KNNLKDCGLF 355

RESULT 12
S28158
GTP-binding regulatory protein Gi alpha-2 chain - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 02-Feb-2001
C;Accession: S28158
R;Sakanaka, C.; Izumi, T.; Nakamura, M.; Honda, Z.; Watanabe, T.; Minami, M.; Mutoh, H.,
Biochim. Biophys. Acta 1175, 61-66, 1992
A;Title: Three types of Gialpha protein of the guinea-pig lung: cDNA cloning and analysi
A;Reference number: S28157; MUID:93129640; PMID:1482697
A;Accession: S28158
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-355 <SAK>
C;Superfamily: GTP-binding regulatory protein Gs alpha chain
C;Keywords: GTP binding; nucleotide binding; P-loop
F;40-47/Region: nucleotide-binding motif A (P-loop)
F;270-273/Region: GTP-binding NKXD motif

  Query Match 100.0%; Score 57; DB 2; Length 355;
  Best Local Similarity 100.0%; Pred. No. 0.0094;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
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Db 346 KNNLKDCGLF 355

RESULT 13
I50238
Gi2 protein alpha-subunit - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50238
R;Kilbourne, E.J.; Galper, J.B.
Gene 150, 341-344, 1994
A;Title: Cloning of cDNAs coding for the G alpha i1 and G alpha i2 G-proteins from chick
A;Reference number: I50237; MUID:95121926; PMID:7821803
A;Accession: I50238
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-355 <KIL>
A;Cross-references: UNIPROT:P50147; GB:L24549; NID:g666872; PIDN:AAA65067.1; PID:g666873
C;Superfamily: GTP-binding regulatory protein Gs alpha chain
C;Keywords: GTP binding; nucleotide binding; P-loop
F;40-47/Region: nucleotide-binding motif A (P-loop)
F;270-273/Region: GTP-binding NKXD motif

Query Match 100.0%; Score 57; DB 2; Length 355;
Best Local Similarity 100.0%; Pred. No. 0.0094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 346 KNNLKDCGLF 355

RESULT 14
A61031
GTP-binding regulatory protein Gi alpha-2 chain (adenylate cyclase-inhibiting) - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A61031
R;Holmer, S.R.; Stevens, S.; Homcy, C.J.
Circ. Res. 65, 1136-1140, 1989
A;Title: Tissue- and species-specific expression of inhibitory guanine nucleotide-bindin
A;Reference number: A61031; MUID:90003652; PMID:2477170
A;Accession: A61031
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-355 <HOL>
A;Cross-references: UNIPROT:P38400
C;Superfamily: GTP-binding regulatory protein Gs alpha chain
C;Keywords: GTP binding; nucleotide binding; P-loop
F;40-47/Region: nucleotide-binding motif A (P-loop)
F;270-273/Region: GTP-binding NKXD motif

Query Match 100.0%; Score 57; DB 2; Length 355;
Best Local Similarity 100.0%; Pred. No. 0.0094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 346 KNNLKDCGLF 355

RESULT 15
A48976
GTP-binding regulatory protein Gi alpha chain - American lobster
C;Species: Homarus americanus (American lobster)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A48976; T01964
R;McClintock, T.S.; Byrnes, A.P.; Lerner, M.R.
Brain Res. Mol. Brain Res. 14, 273-276, 1992
A;Title: Molecular cloning of a G-protein alpha i subunit from the lobster olfactory org
A;Reference number: A48976; MUID:93061797; PMID:1279345
A;Accession: A48976
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-355 <MCC>
A;Cross-references: UNIPROT:P41776; GB:S47614; NID:g259436; PIDN:AAB24072.1; PID:g259437
A;Experimental source: olfactory organ
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:117491, NCBIP:117492)
A;Accession: T01964
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-140,'F',142-307,324-355 <MCW>
A;Cross-references: EMBL:S47614; NID:g259436; PIDN:AAB24072.2; PID:g7330345
C;Superfamily: GTP-binding regulatory protein Gs alpha chain
C;Keywords: GTP binding; nucleotide binding; P-loop
F;41-48/Region: nucleotide-binding motif A (P-loop)
F;270-273/Region: GTP-binding NKXD motif

Query Match 100.0%; Score 57; DB 2; Length 355;
Best Local Similarity 100.0%; Pred. No. 0.0094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 346 KNNLKDCGLF 355

Search completed: March 22, 2005, 06:18:33
Job time : 16 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 22, 2005, 06:00:27 ; Search time 22 Seconds
(without alignments)
33.931 Million cell updates/sec

Title: US-10-009-809-2
Perfect score: 57
Sequence: 1 KNNLKDCGLF 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	57	100.0	10	1	US-08-019-073-19	Sequence 19, Appl
2	57	100.0	10	2	US-08-429-964-50	Sequence 50, Appl
3	57	100.0	10	5	PCT-US93-08062-50	Sequence 50, Appl
4	57	100.0	10	5	PCT-US94-01768-19	Sequence 19, Appl
5	57	100.0	10	6	5428134-6	Patent No. 5428134
6	57	100.0	10	6	5436320-6	Patent No. 5436320
7	57	100.0	10	6	5428134-6	Patent No. 5428134
8	57	100.0	10	6	5436320-6	Patent No. 5436320
9	57	100.0	13	4	US-09-489-156-16	Sequence 16, Appl
10	57	100.0	395	4	US-09-949-016-11560	Sequence 11560, A
11	57	100.0	709	4	US-09-826-509-589	Sequence 589, App
12	51	89.5	10	6	5428134-1	Patent No. 5428134
13	51	89.5	10	6	5428134-10	Patent No. 5428134
14	51	89.5	10	6	5436320-1	Patent No. 5436320
15	51	89.5	10	6	5436320-7	Patent No. 5436320
16	51	89.5	10	6	5428134-1	Patent No. 5428134
17	51	89.5	10	6	5428134-10	Patent No. 5428134
18	51	89.5	10	6	5436320-1	Patent No. 5436320
19	51	89.5	10	6	5436320-7	Patent No. 5436320
20	51	89.5	11	1	US-07-868-353A-7	Sequence 7, Appli
21	51	89.5	11	2	US-08-407-804-7	Sequence 7, Appli
22	51	89.5	11	3	US-09-124-807-7	Sequence 7, Appli
23	51	89.5	13	4	US-09-489-156-15	Sequence 15, Appl
24	51	89.5	40	1	US-07-868-353A-3	Sequence 3, Appli
25	51	89.5	40	2	US-08-407-804-3	Sequence 3, Appli
26	51	89.5	40	3	US-09-124-807-3	Sequence 3, Appli
27	51	89.5	350	1	US-07-868-353A-14	Sequence 14, Appl
28	51	89.5	350	2	US-08-407-804-23	Sequence 23, Appl
29	51	89.5	350	3	US-09-124-807-23	Sequence 23, Appl
30	51	89.5	354	1	US-07-868-353A-12	Sequence 12, Appl
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32	51	89.5	354	1	US-07-868-353A-15	Sequence 15, Appl
33	51	89.5	354	2	US-08-407-804-21	Sequence 21, Appl
34	51	89.5	354	2	US-08-407-804-22	Sequence 22, Appl
35	51	89.5	354	2	US-08-407-804-24	Sequence 24, Appl
36	51	89.5	354	3	US-09-124-807-21	Sequence 21, Appl
37	51	89.5	354	3	US-09-124-807-22	Sequence 22, Appl
38	51	89.5	354	3	US-09-124-807-24	Sequence 24, Appl
39	51	89.5	357	4	US-09-984-292-7	Sequence 7, Appli
40	50	87.7	11	4	US-09-489-156-39	Sequence 39, Appl
41	50	87.7	13	4	US-09-489-156-18	Sequence 18, Appl
42	50	87.7	295	4	US-09-949-016-10678	Sequence 10678, A
43	50	87.7	354	4	US-09-949-016-6727	Sequence 6727, Ap
44	46	80.7	353	4	US-09-984-292-6	Sequence 6, Appli
45	46	80.7	353	4	US-09-984-292-18	Sequence 18, Appl

ALIGNMENTS

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RESULT 1
US-08-019-073-19
; Sequence 19, Application US/08019073
; Patent No. 5559209
;  GENERAL INFORMATION:
;    APPLICANT:  Nishimoto, Ikuo
;    TITLE OF INVENTION:  REGULATOR REGIONS OF G
;    TITLE OF INVENTION:  PROTEINS
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      COMPUTER:  IBM PS/2 Model 50Z or 55SX
;      OPERATING SYSTEM:  MS-DOS (Version 5.0)
;      SOFTWARE:  WordPerfect (Version 5.1)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/019,073
;      FILING DATE:  19930218
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clark, Paul T.
;      REGISTRATION NUMBER:  30,162
;      REFERENCE/DOCKET NUMBER:  00786/146001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-5070
;      TELEFAX:  (617) 542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10
;      TYPE:  AMINO ACID
;      STRANDEDNESS:
;      TOPOLOGY:  linear
US-08-019-073-19

  Query Match             100.0%;  Score 57;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.00037;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 KNNLKDCGLF 10


RESULT 2
US-08-429-964-50
; Sequence 50, Application US/08429964
; Patent No. 5962243
;  GENERAL INFORMATION:
;    APPLICANT:  BROWN, MICHAEL S.
;    APPLICANT:  GOLDSTEIN, JOSEPH L.
;    APPLICANT:  REISS, YUVAL
;    APPLICANT:  JAMES, GUY L.
;    TITLE OF INVENTION:  METHODS FOR THE IDENTIFICATION OF FARNESYL
;    TITLE OF INVENTION:  TRANSFERASE INHIBITORS
;    NUMBER OF SEQUENCES:  85
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ARNOLD, WHITE & DURKEE
;      STREET:  P.O. BOX 4433
;      CITY:  HOUSTON
;      STATE:  TEXAS
;      COUNTRY:  UNITED STATES OF AMERICA
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS/ASCII
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/429,964
;      FILING DATE:  27-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/021,625
;      FILING DATE:  16-FEB-1993
;      CLASSIFICATION:  435
;      APPLICATION NUMBER:  US 07/822,011
;      FILING DATE:  ABANDONED
;      CLASSIFICATION:  435
;      APPLICATION NUMBER:  PCT/US/91/02650
;      FILING DATE:  18-APR-1991
;      CLASSIFICATION:  435
;      APPLICATION NUMBER:  US 07/615,715
;      FILING DATE:  20-NOV-1990
;      CLASSIFICATION:  435
;      APPLICATION NUMBER:  US 07/510,706
;      FILING DATE:  18-APR-1990 (ABANDONED)
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PARKER, DAVID L.
;      REGISTRATION NUMBER:  32,165
;      REFERENCE/DOCKET NUMBER:  UTSD:432/PAR
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (713) 789-2679
;      TELEX:  79-0924
;  INFORMATION FOR SEQ ID NO:  50:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-429-964-50

  Query Match           100.0%;  Score 57;  DB 2;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0.00037;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db          1 KNNLKDCGLF 10


RESULT 3
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PCT-US93-08062-50
; Sequence 50, Application PC/TUS9308062
;  GENERAL INFORMATION:
;    APPLICANT:
;    SEQUENCE CHARACTERISTICS:
;    SEQUENCE CHARACTERISTICS:  BROWN, MICHAEL S.
;    SEQUENCE CHARACTERISTICS:  GOLDSTEIN, JOSEPH L.
;    SEQUENCE CHARACTERISTICS:  REISS, YUVAL
;    SEQUENCE CHARACTERISTICS:  MARSTERS, JR., JAMES C.
;      ADDRESSEE:  METHODS AND COMPOSITIONS FOR
;      ADDRESSEE:  THE IDENTIFICATION,
;      ADDRESSEE:  CHARACTERIZATION AND
;      ADDRESSEE:  INHIBITION OF
;      ADDRESSEE:  FARNESYLTRANSFERASE
;    NUMBER OF SEQUENCES:  71
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ARNOLD, WHITE & DURKEE
;      STREET:  P.O. BOX 4433
;      CITY:  HOUSTON
;      STATE:  TEXAS
;      COUNTRY:  UNITED STATES OF AMERICA
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK/ASKII
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WORDPERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/08062
;      FILING DATE:  AUGUST 24, 1993
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/935,087
;      FILING DATE:  24 AUGUST 1992 (24.08.92)
;      NAME:  UNKNOWN
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PARKER, DAVID L.
;      REGISTRATION NUMBER:  32,165
;      REFERENCE/DOCKET NUMBER:  UTFD377PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  512-320-7200
;      TELEFAX:  512-474-7577
;      TELEX:  NOT APPLICABLE
;  INFORMATION FOR SEQ ID NO:  50:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acid residues
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
PCT-US93-08062-50

  Query Match           100.0%;  Score 57;  DB 5;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0.00037;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db          1 KNNLKDCGLF 10


RESULT 4
PCT-US94-01768-19
; Sequence 19, Application PC/TUS9401768
;  GENERAL INFORMATION:
;    APPLICANT:  Nishimoto, Ikuo
;    TITLE OF INVENTION:  REGULATOR REGIONS OF G PROTEINS
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
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;       ZIP:  02110-2804
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;       COMPUTER:  IBM PS/2 Model 50Z or 55SX
;       OPERATING SYSTEM:  MS-DOS (Version 5.0)
;       SOFTWARE:  WordPerfect (Version 5.1)
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US94/01768
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/019,073
;       FILING DATE:  February 18, 1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Clark, Paul T.
;       REGISTRATION NUMBER:  30,162
;       REFERENCE/DOCKET NUMBER:  00786/146001
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617) 542-5070
;       TELEFAX:  (617) 542-8906
;       TELEX:  200154
;   INFORMATION FOR SEQ ID NO:  19:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  10
;       TYPE:  amino acid
;       STRANDEDNESS:
;       TOPOLOGY:  linear
PCT-US94-01768-19

  Query Match             100.0%;  Score 57;  DB 5;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.00037;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db          1 KNNLKDCGLF 10


RESULT 5
5428134-6
;Patent No. 5428134
;     APPLICANT: Spiegel, Allen M.
;     TITLE OF INVENTION: ANTIBODY REAGENTS THAT SPECIFICALLY
;BIND TO THE CARBOXYL-TERMINAL DECAPTIDE OF SPECIFIC
;GTP-BINDING PROTEINS
;     NUMBER OF SEQUENCES: 11
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/821,849
;       FILING DATE: 14-JAN-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 564,675
;       FILING DATE: 08-AUG-1990
;       APPLICATION NUMBER: 365,919
;       FILING DATE: 15-JAN-1989
;SEQ ID NO:6:
;       LENGTH: 10
5428134-6

  Query Match             100.0%;  Score 57;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.00037;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db          1 KNNLKDCGLF 10


RESULT 6
5436320-6
;Patent No. 5436320
;     APPLICANT: SPIEGEL, ALLEN M.
;     TITLE OF INVENTION: ANTIBODY REAGENTS THAT IDENTIFY THE
;CARBOXY-TERMINAL PEPTIDE OF THE GTP-BINDING PROTEIN G
;     NUMBER OF SEQUENCES: 10
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/820,377
;       FILING DATE: 14-JAN-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 564,675
;       FILING DATE: 08-AUG-1990
;       APPLICATION NUMBER: 365,919
;       FILING DATE: 15-JUN-1989
;       APPLICATION NUMBER: 100,909
;       FILING DATE: 25-SEP-1987
;SEQ ID NO:6:
;       LENGTH: 10
5436320-6

  Query Match             100.0%;  Score 57;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.00037;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db          1 KNNLKDCGLF 10


RESULT 7
5428134-6
;Patent No. 5428134
;     APPLICANT: Spiegel, Allen M.
;     TITLE OF INVENTION: ANTIBODY REAGENTS THAT SPECIFICALLY
;BIND TO THE CARBOXYL-TERMINAL DECAPTIDE OF SPECIFIC
;GTP-BINDING PROTEINS
;     NUMBER OF SEQUENCES: 11
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/821,849
;       FILING DATE: 14-JAN-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 564,675
;       FILING DATE: 08-AUG-1990
;       APPLICATION NUMBER: 365,919
;       FILING DATE: 15-JAN-1989
;SEQ ID NO:6:
;       LENGTH: 10
5428134-6

  Query Match             100.0%;  Score 57;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.00037;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db          1 KNNLKDCGLF 10


RESULT 8
5436320-6
;Patent No. 5436320
;     APPLICANT: SPIEGEL, ALLEN M.
;     TITLE OF INVENTION: ANTIBODY REAGENTS THAT IDENTIFY THE
;CARBOXY-TERMINAL PEPTIDE OF THE GTP-BINDING PROTEIN G
;     NUMBER OF SEQUENCES: 10
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/820,377
;       FILING DATE: 14-JAN-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 564,675
;       FILING DATE: 08-AUG-1990
;       APPLICATION NUMBER: 365,919
;       FILING DATE: 15-JUN-1989
;       APPLICATION NUMBER: 100,909
;       FILING DATE: 25-SEP-1987
;SEQ ID NO:6:
;       LENGTH: 10
5436320-6
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  Query Match            100.0%;  Score 57;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.00037;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db          1 KNNLKDCGLF 10


RESULT 9
US-09-489-156-16
; Sequence 16, Application US/09489156
; Patent No. 6559128
; GENERAL INFORMATION:
;  APPLICANT: HAMM, Heidi
;  APPLICANT:  GILCHRIST, Annette
;  TITLE OF INVENTION: INHIBITORS OF G PROTEIN-MEDIATED SIGNALING, METHODS OF MAKING THE
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: 0290-29 (NU 99037)
;  CURRENT APPLICATION NUMBER: US/09/489,156
;  CURRENT FILING DATE:  2000-01-21
;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
;   LENGTH: 13
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: G alpha i 1/2 peptide
US-09-489-156-16

  Query Match            100.0%;  Score 57;  DB 4;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 0.00049;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db          4 KNNLKDCGLF 13


RESULT 10
US-09-949-016-11560
; Sequence 11560, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11560
;   LENGTH: 395
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-11560

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  Best Local Similarity   100.0%;  Pred. No. 0.017;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
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Db        386 KNNLKDCGLF 395


RESULT 11
US-09-826-509-589
; Sequence 589, Application US/09826509
; Patent No. 6806054
; GENERAL INFORMATION:
;  APPLICANT: Lehmann-Bruinsma, Karin
;  APPLICANT:  Liaw, Chen W.
;  APPLICANT:  Lin, I-Lin
;  TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
;  TITLE OF INVENTION:  Protein-Coupled Receptors
;  FILE REFERENCE: AREN-207
;  CURRENT APPLICATION NUMBER: US/09/826,509
;  CURRENT FILING DATE:  2001-04-05
;  PRIOR APPLICATION NUMBER: 60/195,747
;  PRIOR FILING DATE: 2000-04-07
;  PRIOR APPLICATION NUMBER: 09/170,496
;  PRIOR FILING DATE: 1998-10-13
;  NUMBER OF SEQ ID NOS: 589
;  SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 589
;   LENGTH: 709
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-826-509-589

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  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
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Db        700 KNNLKDCGLF 709


RESULT 12
5428134-1
;Patent No. 5428134
;    APPLICANT: Spiegel, Allen M.
;    TITLE OF INVENTION: ANTIBODY REAGENTS THAT SPECIFICALLY
;BIND TO THE CARBOXYL-TERMINAL DECAPTIDE OF SPECIFIC
;GTP-BINDING PROTEINS
;    NUMBER OF SEQUENCES: 11
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/821,849
;      FILING DATE: 14-JAN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 564,675
;      FILING DATE: 08-AUG-1990
;      APPLICATION NUMBER: 365,919
;      FILING DATE: 15-JAN-1989
;SEQ ID NO:1:
;      LENGTH: 10
5428134-1

  Query Match            89.5%;  Score 51;  DB 6;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 0.0045;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              | ||||||||
Db          1 KENLKDCGLF 10


RESULT 13
5428134-10
;Patent No. 5428134
;    APPLICANT: Spiegel, Allen M.
;    TITLE OF INVENTION: ANTIBODY REAGENTS THAT SPECIFICALLY
;BIND TO THE CARBOXYL-TERMINAL DECAPTIDE OF SPECIFIC
;GTP-BINDING PROTEINS
;    NUMBER OF SEQUENCES: 11
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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/821,849
;      FILING DATE: 14-JAN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 564,675
;      FILING DATE: 08-AUG-1990
;      APPLICATION NUMBER: 365,919
;      FILING DATE: 15-JAN-1989
;SEQ ID NO:10:
;      LENGTH: 10
5428134-10

  Query Match             89.5%;  Score 51;  DB 6;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 0.0045;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              | ||||||||
Db          1 KENLKDCGLF 10


RESULT 14
5436320-1
;Patent No. 5436320
;    APPLICANT: SPIEGEL, ALLEN M.
;    TITLE OF INVENTION: ANTIBODY REAGENTS THAT IDENTIFY THE
;CARBOXY-TERMINAL PEPTIDE OF THE GTP-BINDING PROTEIN G
;    NUMBER OF SEQUENCES: 10
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/820,377
;      FILING DATE: 14-JAN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 564,675
;      FILING DATE: 08-AUG-1990
;      APPLICATION NUMBER: 365,919
;      FILING DATE: 15-JUN-1989
;      APPLICATION NUMBER: 100,909
;      FILING DATE: 25-SEP-1987
;SEQ ID NO:1:
;      LENGTH: 10
5436320-1

  Query Match             89.5%;  Score 51;  DB 6;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 0.0045;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              | ||||||||
Db          1 KENLKDCGLF 10


RESULT 15
5436320-7
;Patent No. 5436320
;    APPLICANT: SPIEGEL, ALLEN M.
;    TITLE OF INVENTION: ANTIBODY REAGENTS THAT IDENTIFY THE
;CARBOXY-TERMINAL PEPTIDE OF THE GTP-BINDING PROTEIN G
;    NUMBER OF SEQUENCES: 10
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/820,377
;      FILING DATE: 14-JAN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 564,675
;      FILING DATE: 08-AUG-1990
;      APPLICATION NUMBER: 365,919
;      FILING DATE: 15-JUN-1989
;      APPLICATION NUMBER: 100,909
;      FILING DATE: 25-SEP-1987
;SEQ ID NO:7:
;      LENGTH: 10
5436320-7

  Query Match             89.5%;  Score 51;  DB 6;  Length 10;
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  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
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Db          1 KENLKDCGLF 10


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Job time : 23 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 22, 2005, 06:30:50 ; Search time 139 Seconds
(without alignments)
23.780 Million cell updates/sec

Title: US-10-009-809-2
Perfect score: 57
Sequence: 1 KNNLKDCGLF 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	57	100.0	10	16	US-10-465-826-31	Sequence 31, Appl
2	57	100.0	11	10	US-09-852-910-17	Sequence 17, Appl
3	57	100.0	11	15	US-10-411-336A-17	Sequence 17, Appl
4	57	100.0	13	10	US-09-852-910-112	Sequence 112, App
5	57	100.0	13	14	US-10-373-540-16	Sequence 16, Appl
6	57	100.0	13	15	US-10-411-336A-112	Sequence 112, App
7	57	100.0	339	15	US-10-108-260A-3642	Sequence 3642, Ap
8	57	100.0	339	15	US-10-108-260A-3821	Sequence 3821, Ap
9	57	100.0	353	15	US-10-059-266B-18	Sequence 18, Appl
10	57	100.0	354	10	US-09-952-680A-19	Sequence 19, Appl
11	57	100.0	354	15	US-10-352-843-14	Sequence 14, Appl
12	57	100.0	354	15	US-10-059-266B-4	Sequence 4, Appli
13	57	100.0	355	9	US-09-947-953-2	Sequence 2, Appli
14	57	100.0	355	10	US-09-952-680A-20	Sequence 20, Appl
15	57	100.0	355	10	US-09-952-680A-23	Sequence 23, Appl
16	57	100.0	355	15	US-10-116-275-267	Sequence 267, App
17	57	100.0	355	16	US-10-408-765A-427	Sequence 427, App
18	57	100.0	355	16	US-10-408-765A-2392	Sequence 2392, Ap
19	57	100.0	695	17	US-10-491-654-23	Sequence 23, Appl
20	57	100.0	709	10	US-09-826-509-589	Sequence 589, App
21	57	100.0	709	17	US-10-925-095-589	Sequence 589, App
22	53	93.0	10	16	US-10-465-826-4	Sequence 4, Appli
23	53	93.0	26	16	US-10-465-826-10	Sequence 10, Appl
24	53	93.0	26	16	US-10-465-826-19	Sequence 19, Appl
25	51	89.5	10	16	US-10-465-826-2	Sequence 2, Appli
26	51	89.5	11	10	US-09-789-996-7	Sequence 7, Appli
27	51	89.5	11	10	US-09-852-910-15	Sequence 15, Appl
28	51	89.5	11	15	US-10-411-336A-15	Sequence 15, Appl
29	51	89.5	13	14	US-10-373-540-15	Sequence 15, Appl
30	51	89.5	26	16	US-10-465-826-25	Sequence 25, Appl
31	51	89.5	40	10	US-09-789-996-3	Sequence 3, Appli
32	51	89.5	157	10	US-09-952-680A-33	Sequence 33, Appl
33	51	89.5	350	10	US-09-789-996-23	Sequence 23, Appl
34	51	89.5	350	10	US-09-952-680A-24	Sequence 24, Appl
35	51	89.5	350	15	US-10-352-843-15	Sequence 15, Appl
36	51	89.5	350	15	US-10-380-393B-1	Sequence 1, Appli
37	51	89.5	350	15	US-10-059-266B-8	Sequence 8, Appli
38	51	89.5	350	16	US-10-408-765A-428	Sequence 428, App
39	51	89.5	354	10	US-09-789-996-21	Sequence 21, Appl
40	51	89.5	354	10	US-09-789-996-22	Sequence 22, Appl
41	51	89.5	354	10	US-09-789-996-24	Sequence 24, Appl
42	51	89.5	354	10	US-09-952-680A-25	Sequence 25, Appl
43	51	89.5	357	9	US-09-984-292-7	Sequence 7, Appli
44	51	89.5	357	9	US-09-989-497-7	Sequence 7, Appli
45	50	87.7	10	16	US-10-465-826-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-10-465-826-31
; Sequence 31, Application US/10465826
; Publication No. US20040137006A1
; GENERAL INFORMATION:
; APPLICANT: ALLERGENE LTD.
; APPLICANT: Eisenberg, Ronit
; APPLICANT: Raz, Tamar
; TITLE OF INVENTION: ANTI-ALLERGIC COMPLEX MOLECULES
; FILE REFERENCE: ALL/002 US
; CURRENT APPLICATION NUMBER: US/10/465,826
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: PCT/IL01/01186
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-465-826-31

Query Match 100.0%; Score 57; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 KNNLKDCGLF 10
              ||||||||||
Db          1 KNNLKDCGLF 10
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RESULT 2
US-09-852-910-17
; Sequence 17, Application US/09852910
; Publication No. US20030096297A1
; GENERAL INFORMATION:

```
;  APPLICANT: Hamm, Heidi
;  APPLICANT:  Gilchrist, Annette
;  TITLE OF INVENTION: Method For Identifying Inhibitors of G Protein Coupled Receptor S
;  FILE REFERENCE: 2661-101
;  CURRENT APPLICATION NUMBER: US/09/852,910
;  CURRENT FILING DATE:  2001-09-18
;  PRIOR APPLICATION NUMBER: US 60/275,472
;  PRIOR FILING DATE: 2001-03-14
;  NUMBER OF SEQ ID NOS: 271
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-852-910-17

  Query Match           100.0%;  Score 57;  DB 10;  Length 11;
  Best Local Similarity  100.0%;  Pred. No. 0.0014;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db          2 KNNLKDCGLF 11


RESULT 3
US-10-411-336A-17
; Sequence 17, Application US/10411336A
; Publication No. US20040018558A1
; GENERAL INFORMATION:
;  APPLICANT: GILCHRIST, ANNETTE
;  APPLICANT:  HAMM, HEIDI
;  TITLE OF INVENTION: METHOD FOR IDENTIFYING MODULATORS OF G PROTEIN COUPLED RECEPTOR
;  TITLE OF INVENTION:  SIGNALING
;  FILE REFERENCE: 2661-102
;  CURRENT APPLICATION NUMBER: US/10/411,336A
;  CURRENT FILING DATE:  2003-04-11
;  PRIOR APPLICATION NUMBER: US 09/852910
;  PRIOR FILING DATE: 2001-05-11
;  PRIOR APPLICATION NUMBER: US 60/275472
;  PRIOR FILING DATE: 2001-03-14
;  NUMBER OF SEQ ID NOS: 273
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-411-336A-17

  Query Match           100.0%;  Score 57;  DB 15;  Length 11;
  Best Local Similarity  100.0%;  Pred. No. 0.0014;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db          2 KNNLKDCGLF 11


RESULT 4
US-09-852-910-112
; Sequence 112, Application US/09852910
; Publication No. US20030096297A1
; GENERAL INFORMATION:
;  APPLICANT: Hamm, Heidi
;  APPLICANT:  Gilchrist, Annette
;  TITLE OF INVENTION: Method For Identifying Inhibitors of G Protein Coupled Receptor S
;  FILE REFERENCE: 2661-101
;  CURRENT APPLICATION NUMBER: US/09/852,910
;  CURRENT FILING DATE:  2001-09-18
;  PRIOR APPLICATION NUMBER: US 60/275,472
;  PRIOR FILING DATE: 2001-03-14
;  NUMBER OF SEQ ID NOS: 271
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 112
;   LENGTH: 13
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(13)
;   OTHER INFORMATION: G alpha i minigene peptide
US-09-852-910-112

  Query Match           100.0%;  Score 57;  DB 10;  Length 13;
  Best Local Similarity  100.0%;  Pred. No. 0.0016;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db          4 KNNLKDCGLF 13


RESULT 5
US-10-373-540-16
; Sequence 16, Application US/10373540
; Publication No. US20030162258A1
; GENERAL INFORMATION:
;  APPLICANT: HAMM, Heidi
;  APPLICANT:  GILCHRIST, Annette
;  TITLE OF INVENTION: INHIBITORS OF G PROTEIN-MEDIATED SIGNALING, METHODS OF MAKING TH
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: 0290-29 (NU 99037)
;  CURRENT APPLICATION NUMBER: US/10/373,540
;  CURRENT FILING DATE:  2003-02-24
;  PRIOR APPLICATION NUMBER: US/09/489,156
;  PRIOR FILING DATE: PRIOR  FILING DATE:  2000-01-21
;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
;   LENGTH: 13
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: G alpha i 1/2 peptide
US-10-373-540-16

  Query Match           100.0%;  Score 57;  DB 14;  Length 13;
  Best Local Similarity  100.0%;  Pred. No. 0.0016;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db          4 KNNLKDCGLF 13


RESULT 6
US-10-411-336A-112
; Sequence 112, Application US/10411336A
; Publication No. US20040018558A1
; GENERAL INFORMATION:
;  APPLICANT: GILCHRIST, ANNETTE
;  APPLICANT:  HAMM, HEIDI
;  TITLE OF INVENTION: METHOD FOR IDENTIFYING MODULATORS OF G PROTEIN COUPLED RECEPTOR
;  TITLE OF INVENTION:  SIGNALING
;  FILE REFERENCE: 2661-102
;  CURRENT APPLICATION NUMBER: US/10/411,336A
;  CURRENT FILING DATE:  2003-04-11
;  PRIOR APPLICATION NUMBER: US 09/852910
;  PRIOR FILING DATE: 2001-05-11
;  PRIOR APPLICATION NUMBER: US 60/275472
;  PRIOR FILING DATE: 2001-03-14
;  NUMBER OF SEQ ID NOS: 273
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 112
;   LENGTH: 13
;   TYPE: PRT
```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: G alpha i minigene peptide
US-10-411-336A-112

Query Match 100.0%; Score 57; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 4 KNNLKDCGLF 13

RESULT 7
US-10-108-260A-3642
; Sequence 3642, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3642
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-3642

Query Match 100.0%; Score 57; DB 15; Length 339;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 330 KNNLKDCGLF 339

RESULT 8
US-10-108-260A-3821
; Sequence 3821, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3821
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-3821

Query Match 100.0%; Score 57; DB 15; Length 339;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 330 KNNLKDCGLF 339

RESULT 9
US-10-059-266B-18
; Sequence 18, Application US/10059266B
; Publication No. US20040072157A1
; GENERAL INFORMATION:
; APPLICANT: Graber, Stephen G.
; TITLE OF INVENTION: Soluble Chimeric G Protein Alpha Subunits
; FILE REFERENCE: 033524-001
; CURRENT APPLICATION NUMBER: US/10/059,266B
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 60/265,068
; PRIOR FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Gqil131N25C alpha subunit
US-10-059-266B-18

Query Match 100.0%; Score 57; DB 15; Length 353;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 344 KNNLKDCGLF 353

RESULT 10
US-09-952-680A-19
; Sequence 19, Application US/09952680A
; Publication No. US20030087239A1
; GENERAL INFORMATION:
; APPLICANT: Stanton, Marty
; APPLICANT: Epstein, David
; APPLICANT: Hamaguchi, No. US20030087239A1uko
; TITLE OF INVENTION: Target Activated Biosensor and Methods of Using Same
; FILE REFERENCE: 23239-501
; CURRENT APPLICATION NUMBER: US/09/952,680A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,454
; PRIOR FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-952-680A-19

Query Match 100.0%; Score 57; DB 10; Length 354;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 345 KNNLKDCGLF 354

RESULT 11
US-10-352-843-14
; Sequence 14, Application US/10352843
; Publication No. US20040014135A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Lisa
; APPLICANT: Kindt, Rachel
; APPLICANT: Kopczynski, Jenny
; APPLICANT: Doberstein, Stephen
; APPLICANT: Cockett, Mark
; APPLICANT: Ramanathan, Chandra
; APPLICANT: Lodge, Nicholas
; APPLICANT: Fitzgerald, Kevin
; APPLICANT: Stouch, Terry
; TITLE OF INVENTION: MOLECULES THAT MODULATE G(ALPHA)q ACTIVITY AND METHODS OF
; TITLE OF INVENTION: TREATING URINARY INCONTINENCE

```
;  FILE REFERENCE: 5624-277-999
;  CURRENT APPLICATION NUMBER: US/10/352,843
;  CURRENT FILING DATE:  2003-01-27
;  PRIOR APPLICATION NUMBER: US 60/352720
;  PRIOR FILING DATE: 2003-01-27
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
;   LENGTH: 354
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: G-protein of the invention
US-10-352-843-14

  Query Match             100.0%;  Score 57;  DB 15;  Length 354;
  Best Local Similarity   100.0%;  Pred. No. 0.045;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        345 KNNLKDCGLF 354


RESULT 12
US-10-059-266B-4
; Sequence 4, Application US/10059266B
; Publication No. US20040072157A1
; GENERAL INFORMATION:
;  APPLICANT: Graber, Stephen G.
;  TITLE OF INVENTION: Soluble Chimeric G Protein Alpha Subunits
;  FILE REFERENCE: 033524-001
;  CURRENT APPLICATION NUMBER: US/10/059,266B
;  CURRENT FILING DATE:  2002-01-31
;  PRIOR APPLICATION NUMBER: US 60/265,068
;  PRIOR FILING DATE: 2001-01-31
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 354
;   TYPE: PRT
;   ORGANISM: Rat
US-10-059-266B-4

  Query Match             100.0%;  Score 57;  DB 15;  Length 354;
  Best Local Similarity   100.0%;  Pred. No. 0.045;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        345 KNNLKDCGLF 354


RESULT 13
US-09-947-953-2
; Sequence 2, Application US/09947953
; Patent No. US20020155101A1
; GENERAL INFORMATION:
;  APPLICANT: DONAHUE, J. KEVIN
;  APPLICANT:  MARBAN, EDUARDO
;  TITLE OF INVENTION: CARDIAC ARRHYTHMIA TREATMENT METHODS
;  FILE REFERENCE: 71699/56415
;  CURRENT APPLICATION NUMBER: US/09/947,953
;  CURRENT FILING DATE:  2001-09-06
;  PRIOR APPLICATION NUMBER: 60/230,311
;  PRIOR FILING DATE: 2001-09-06
;  PRIOR APPLICATION NUMBER: 60/295,889
;  PRIOR FILING DATE: 2001-06-05
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 355
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-947-953-2

  Query Match             100.0%;  Score 57;  DB 9;  Length 355;
  Best Local Similarity   100.0%;  Pred. No. 0.046;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        346 KNNLKDCGLF 355


RESULT 14
US-09-952-680A-20
; Sequence 20, Application US/09952680A
; Publication No. US20030087239A1
; GENERAL INFORMATION:
;  APPLICANT: Stanton, Marty
;  APPLICANT:  Epstein, David
;  APPLICANT:  Hamaguchi, No. US20030087239A1uko
;  TITLE OF INVENTION: Target Activated Biosensor and Methods of Using Same
;  FILE REFERENCE: 23239-501
;  CURRENT APPLICATION NUMBER: US/09/952,680A
;  CURRENT FILING DATE:  2001-09-13
;  PRIOR APPLICATION NUMBER: 60/232,454
;  PRIOR FILING DATE: 2000-09-13
;  NUMBER OF SEQ ID NOS: 75
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
;   LENGTH: 355
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-952-680A-20

  Query Match             100.0%;  Score 57;  DB 10;  Length 355;
  Best Local Similarity   100.0%;  Pred. No. 0.046;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        346 KNNLKDCGLF 355


RESULT 15
US-09-952-680A-23
; Sequence 23, Application US/09952680A
; Publication No. US20030087239A1
; GENERAL INFORMATION:
;  APPLICANT: Stanton, Marty
;  APPLICANT:  Epstein, David
;  APPLICANT:  Hamaguchi, No. US20030087239A1uko
;  TITLE OF INVENTION: Target Activated Biosensor and Methods of Using Same
;  FILE REFERENCE: 23239-501
;  CURRENT APPLICATION NUMBER: US/09/952,680A
;  CURRENT FILING DATE:  2001-09-13
;  PRIOR APPLICATION NUMBER: 60/232,454
;  PRIOR FILING DATE: 2000-09-13
;  NUMBER OF SEQ ID NOS: 75
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
;   LENGTH: 355
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-952-680A-23

  Query Match             100.0%;  Score 57;  DB 10;  Length 355;
  Best Local Similarity   100.0%;  Pred. No. 0.046;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        346 KNNLKDCGLF 355
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```
RESULT 16
US-10-116-275-267
; Sequence 267, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
;  APPLICANT: Elan Pharmaceutical Technology
;  APPLICANT:  O'Mahony, Daniel J.
;  APPLICANT:  Brayden, David
;  APPLICANT:  Byrne, Daragh
;  APPLICANT:  Lambkin, Imelda
;  APPLICANT:  Higgins, Lisa
;  TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
;  TITLE OF INVENTION:  Compositions Targeting Peyer's Patches and M Cell Receptors
;  FILE REFERENCE: E1067/20087
;  CURRENT APPLICATION NUMBER: US/10/116,275
;  CURRENT FILING DATE:  2002-10-04
;  NUMBER OF SEQ ID NOS: 349
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 267
;   LENGTH: 355
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-116-275-267

  Query Match             100.0%;  Score 57;  DB 15;  Length 355;
  Best Local Similarity   100.0%;  Pred. No. 0.046;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        346 KNNLKDCGLF 355


RESULT 17
US-10-408-765A-427
; Sequence 427, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
;  APPLICANT: Ghosh, Soumitra S.
;  APPLICANT:  Fahy, Eoin D.
;  APPLICANT:  Zhang, Bing
;  APPLICANT:  Gibson, Bradford W.
;  APPLICANT:  Taylor, Steven W.
;  APPLICANT:  Glenn, Gary M.
;  APPLICANT:  Warnock, Dale E.
;  TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
;  TITLE OF INVENTION:  IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
;  FILE REFERENCE: 660088.465
;  CURRENT APPLICATION NUMBER: US/10/408,765A
;  CURRENT FILING DATE:  2003-04-04
;  NUMBER OF SEQ ID NOS: 3077
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 427
;   LENGTH: 355
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-408-765A-427

  Query Match             100.0%;  Score 57;  DB 16;  Length 355;
  Best Local Similarity   100.0%;  Pred. No. 0.046;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        346 KNNLKDCGLF 355


RESULT 18
US-10-408-765A-2392
; Sequence 2392, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
;  APPLICANT: Ghosh, Soumitra S.
;  APPLICANT:  Fahy, Eoin D.
;  APPLICANT:  Zhang, Bing
;  APPLICANT:  Gibson, Bradford W.
;  APPLICANT:  Taylor, Steven W.
;  APPLICANT:  Glenn, Gary M.
;  APPLICANT:  Warnock, Dale E.
;  TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
;  TITLE OF INVENTION:  IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
;  FILE REFERENCE: 660088.465
;  CURRENT APPLICATION NUMBER: US/10/408,765A
;  CURRENT FILING DATE:  2003-04-04
;  NUMBER OF SEQ ID NOS: 3077
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2392
;   LENGTH: 355
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-408-765A-2392

  Query Match             100.0%;  Score 57;  DB 16;  Length 355;
  Best Local Similarity   100.0%;  Pred. No. 0.046;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        346 KNNLKDCGLF 355


RESULT 19
US-10-491-654-23
; Sequence 23, Application US/10491654
; Publication No. US20050014689A1
; GENERAL INFORMATION:
;  APPLICANT: SUGARU, Eiji
;  APPLICANT:  TSUCHIDA, Atsushi
;  APPLICANT:  YAMANAKA, Mitsugu
;  APPLICANT:  TAIJI, Mutsuo
;  TITLE OF INVENTION: REMEDIES FOR LIFE STYLE-RELATED DISEASES OR CIBOPHOBIA
;  TITLE OF INVENTION:  AND METHOD OF SCREENING THE SAME
;  FILE REFERENCE: 228328
;  CURRENT APPLICATION NUMBER: US/10/491,654
;  CURRENT FILING DATE:  2004-04-02
;  PRIOR APPLICATION NUMBER: PCT/JP02/10250
;  PRIOR FILING DATE: 2002-10-02
;  PRIOR APPLICATION NUMBER: JP 2001-306872
;  PRIOR FILING DATE: 2001-10-02
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 23
;   LENGTH: 695
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Insert cDNA sequence contained in pc901HISG-alpha-i2.
US-10-491-654-23

  Query Match             100.0%;  Score 57;  DB 17;  Length 695;
  Best Local Similarity   100.0%;  Pred. No. 0.09;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        686 KNNLKDCGLF 695


RESULT 20
US-09-826-509-589
; Sequence 589, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
;  APPLICANT: Lehmann-Bruinsma, Karin
;  APPLICANT:  Liaw, Chen W.
```

```
;  APPLICANT:  Lin, I-Lin
;  TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
;  TITLE OF INVENTION:  Protein-Coupled Receptors
;  FILE REFERENCE: AREN-207
;  CURRENT APPLICATION NUMBER: US/09/826,509
;  CURRENT FILING DATE:  2001-04-05
;  PRIOR APPLICATION NUMBER: 60/195,747
;  PRIOR FILING DATE: 2000-04-07
;  PRIOR APPLICATION NUMBER: 09/170,496
;  PRIOR FILING DATE: 1998-10-13
;  NUMBER OF SEQ ID NOS: 589
;  SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 589
;   LENGTH: 709
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-826-509-589

  Query Match             100.0%;  Score 57;  DB 10;  Length 709;
  Best Local Similarity   100.0%;  Pred. No. 0.092;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        700 KNNLKDCGLF 709


RESULT 21
US-10-925-095-589
; Sequence 589, Application US/10925095
; Publication No. US20050019840A1
; GENERAL INFORMATION:
;  APPLICANT: Lehmann-Bruinsma, Karin
;  APPLICANT:  Liaw, Chen W.
;  APPLICANT:  Lin, I-Lin
;  TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Known G
;  TITLE OF INVENTION:  Protein-Coupled Receptors
;  FILE REFERENCE: AREN-207
;  CURRENT APPLICATION NUMBER: US/10/925,095
;  CURRENT FILING DATE:  2004-08-24
;  PRIOR APPLICATION NUMBER: US/09/826,509
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/195,747
;  PRIOR FILING DATE: 2000-04-07
;  PRIOR APPLICATION NUMBER: 09/170,496
;  PRIOR FILING DATE: 1998-10-13
;  NUMBER OF SEQ ID NOS: 589
;  SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 589
;   LENGTH: 709
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-925-095-589

  Query Match             100.0%;  Score 57;  DB 17;  Length 709;
  Best Local Similarity   100.0%;  Pred. No. 0.092;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        700 KNNLKDCGLF 709


Search completed: March 22, 2005, 06:44:06
Job time : 139 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 22, 2005, 06:31:49 ; Search time 164 Seconds
(without alignments)
23.583 Million cell updates/sec

Title: US-10-009-809-2
Perfect score: 57
Sequence: 1 KNNLKDCGLF 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 50

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 500 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	57	100.0	10	2	AAR61259	Aar61259 Control p
2	57	100.0	10	2	AAR49785	Aar49785 Farnesylt
3	57	100.0	10	2	AAW04476	Aaw04476 Weak inhi
4	57	100.0	10	5	AAE26151	Aae26151 Galphai2
5	57	100.0	11	6	ABJ36692	Abj36692 G protein
6	57	100.0	13	6	ABJ36771	Abj36771 G protein
7	57	100.0	13	7	ABW00010	Abw00010 Human G a
8	57	100.0	13	7	ADF45264	Adf45264 G alpha c
9	57	100.0	23	4	AAO08372	Aao08372 Human pol
10	57	100.0	26	4	AAY72144	Aay72144 Modified
11	57	100.0	27	4	AAY72145	Aay72145 Anti-alle
12	57	100.0	288	6	ABR41313	Abr41313 Human DIT
13	57	100.0	339	7	ADM05136	Adm05136 Human pro
14	57	100.0	339	7	ADM04957	Adm04957 Human pro
15	57	100.0	353	7	ADE57521	Ade57521 Human Pro
16	57	100.0	353	7	ADE57515	Ade57515 Rat Prote
17	57	100.0	353	7	ADE57517	Ade57517 Human Pro
18	57	100.0	353	7	ADE57519	Ade57519 Rat Prote
19	57	100.0	353	8	ADN06152	Adn06152 Rat Gi1-H
20	57	100.0	354	3	AAY85290	Aay85290 Human G-a
21	57	100.0	354	4	AAB99064	Aab99064 Human G-p
22	57	100.0	354	5	ABB09273	Abb09273 G protein
23	57	100.0	354	7	ABR82632	Abr82632 C. elegan
24	57	100.0	354	7	ADC09608	Adc09608 Human G-p
25	57	100.0	354	7	ADE59387	Ade59387 Human Pro
26	57	100.0	354	7	ADE59391	Ade59391 Human Pro
27	57	100.0	354	7	ADE59385	Ade59385 Rat Prote
28	57	100.0	354	7	ADE59389	Ade59389 Rat Prote
29	57	100.0	354	7	ADD46017	Add46017 Human Pro
30	57	100.0	354	8	ADN06138	Adn06138 Rat Gi1 a
31	57	100.0	354	8	ADQ08808	Adq08808 Ciona int
32	57	100.0	355	3	AAY85149	Aay85149 Human G-a
33	57	100.0	355	4	AAB99065	Aab99065 Human G-p
34	57	100.0	355	5	ABB09274	Abb09274 G protein
35	57	100.0	355	5	ABB09277	Abb09277 G protein
36	57	100.0	355	5	AAU79335	Aau79335 Human inh
37	57	100.0	355	7	ADC09612	Adc09612 Human G-p
38	57	100.0	355	7	ADC09609	Adc09609 Human G-p
39	57	100.0	355	7	ADJ68621	Adj68621 Human hea
40	57	100.0	355	7	ADJ70586	Adj70586 Human hea
41	57	100.0	355	7	ADP70781	Adp70781 Minicell
42	57	100.0	355	8	ADM67196	Adm67196 Human adi
43	57	100.0	355	8	ABM80456	Abm80456 Tumour-as
44	57	100.0	362	8	ADG36979	Adg36979 Human GPC
45	57	100.0	695	6	ABR56305	Abr56305 pc901HISG
46	57	100.0	709	4	ABB56396	Abb56396 TSHR-Gs-a
47	57	100.0	709	6	ABR55447	Abr55447 Amino aci
48	57	100.0	725	4	AAB99036	Aab99036 Human som
49	57	100.0	784	7	ADG37260	Adg37260 Fusion co
50	57	100.0	987	7	ADC51269	Adc51269 Chimeric

ALIGNMENTS

RESULT 1
AAR61259
ID AAR61259 standard; peptide; 10 AA.
XX
AC AAR61259;
XX
DT 25-MAR-2003 (revised)
DT 13-APR-1995 (first entry)
XX
DE Control peptide corresponding to Gi2 alpha Lys346-Phe355.
XX
KW Anticouplone; G-protein; Regulator region; Immunosuppressant.
XX
OS Synthetic.
XX
PN WO9419002-A1.
XX
PD 01-SEP-1994.
XX
PF 17-FEB-1994; 94WO-US001768.
XX
PR 18-FEB-1993; 93US-00019073.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Nishimoto I;
XX
DR WPI; 1994-293996/36.
XX
PT Anticouplone sequences of G proteins - inhibit activation of G protein by
PT G-coupled receptor, used to treat neuromuscular and autoimmune diseases,
PT cancer, diabetes, hypertension, AIDS etc.
XX
PS Disclosure; Page 8; 52pp; English.
XX
CC Control peptide, showed no effect on peptide (AAR61267) induced Gi2
CC activation. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 57; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 KNNLKDCGLF 10
              ||||||||||
Db          1 KNNLKDCGLF 10
```

RESULT 2
AAR49785
ID AAR49785 standard; peptide; 10 AA.
XX
AC AAR49785;
XX
DT 25-MAR-2003 (revised)
DT 08-AUG-1994 (first entry)
XX
DE Farnesyltransferase-inhibitor.
XX
KW Farnesyltransferase-inhibitor; farnesyltransferase; FT; p21ras;
KW ras protein; farnesylation; cancer therapy.
XX
OS Synthetic.
XX
PN WO9404561-A1.
XX
PD 03-MAR-1994.
XX
PF 24-AUG-1993; 93WO-US008062.
XX
PR 24-AUG-1992; 92US-00935087.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
PA (GETH) GENENTECH INC.
XX
PI Brown MS, Goldstein JL, Reiss Y, Marsters JC;
XX
DR WPI; 1994-083105/10.
XX
PT New farnesyl-transferase inhibitors - used for inhibiting attachment of a
PT farnesyl moiety to a p21ras protein in malignant cells.
XX
PS Disclosure; Page 49; 183pp; English.
XX
CC Peptides given in AAR49741-75, AAR49777-78 and AAR49785-88, which include
CC a family of tetrapeptides based on the recognition site (AAR49776) of
CC farnesyltransferase (FT), are potential anticancer agents that inhibit
CC FT, thereby preventing expression of p21ras. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 10 AA;

  Query Match   100.0%; Score 57; DB 2; Length 10;
  Best Local Similarity   100.0%; Pred. No. 0.0013;
  Matches   10; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy          1 KNNLKDCGLF 10
              ||||||||||
Db          1 KNNLKDCGLF 10
```

RESULT 3
AAW04476
ID AAW04476 standard; peptide; 10 AA.
XX
AC AAW04476;
XX
DT 05-AUG-1997 (first entry)
XX
DE Weak inhibitor of farnesyl transferase.
XX
KW Farnesyl transferase; inhibitor; cancer; tumour; neoplasia; prenyl;
KW ras protein; K-ras B; malignant; detection; identification.
XX
OS Synthetic.
XX
PN WO9634113-A2.
XX
PD 31-OCT-1996.
XX
PF 29-APR-1996; 96WO-US005969.
XX
PR 27-APR-1995; 95US-00429964.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Brown MS, Goldstein JL, James GL;
XX
DR WPI; 1996-497642/49.
XX
PT Assay for farnesyl transferase activity - by determining ability to
PT transfer farnesyl moiety to K-Ras B protein, partic. useful for
PT identifying inhibitors.
XX
PS Disclosure; Page 179; 257pp; English.
XX
CC AAW04476-W04478 are weak peptide inhibitors of farnesyl transferase (FT)
CC activity. FT peptide inhibitors block the attachment of prenyl groups to
CC ras proteins in malignant cells of patients suffering from cancer or a
CC precancerous state and as such are used to treat cancer. The peptides
CC were identified by determining the ability of candidate substances to
CC inhibit a FT enzyme, by inhibiting the transfer of a farnesyl moiety to a
CC K-Ras B protein
XX
SQ Sequence 10 AA;

  Query Match   100.0%; Score 57; DB 2; Length 10;
  Best Local Similarity   100.0%; Pred. No. 0.0013;
  Matches   10; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy          1 KNNLKDCGLF 10
              ||||||||||
Db          1 KNNLKDCGLF 10
```

RESULT 4
AAE26151
ID AAE26151 standard; peptide; 10 AA.
XX
AC AAE26151;
XX
DT 14-NOV-2002 (first entry)
XX
DE Galphai2 peptide, peptide b.
XX
KW Antiallergic agent; nasal allergy; eye; skin; acute urticaria; psoriasis;
KW psychogenic; allergic asthma; interstitial cystitis; bowel disease;
KW multiple sclerosis; dermatological; antiinflammatory; neuroprotective;
KW migraine.
XX
OS Unidentified.
XX
PN WO200250097-A2.
XX
PD 27-JUN-2002.
XX
PF 20-DEC-2001; 2001WO-IL001186.
XX
PR 21-DEC-2000; 2000IL-00140473.
XX
PA (ALLE-) ALLERGENE LTD.
XX
PI Eisenberg R, Raz T;
XX
DR WPI; 2002-636474/68.
XX
PT New antiallergic agent having first cell penetrating segment joined to
PT antiallergic decapeptide providing antiallergic effect within mast cells,

PT through linker which provides bend or turn at junction between segments.
XX
PS Example 7; Page 51; 81pp; English.
XX
CC The invention relates to an antiallergic agent, comprising a complex
CC molecule having at least a first segment competent for importation of the
CC molecule into mast cells, joined to a second segment through a linker,
CC where the second segment is the anti-allergic decapeptide derived from
CC Galphai_3, providing antiallergic effect within mast cells, and linker
CC provides a bend or turn at or near junction between the two segments. The
CC invention is useful for treating allergic conditions such as nasal
CC allergy, allergic reactions in an eye of the subject, allergic reactions
CC in the skin of the subject, acute urticaria, psoriasis, psychogenic or
CC allergic asthma, interstitial cystitis, bowel diseases, migraines or
CC multiple sclerosis. The invention is also useful for preventing late
CC phase inflammatory responses induced by protein kinase activation,
CC preferably mitogen activated protein kinase activation, where the
CC antiallergic agent is peptide 2, peptide 2-Succ and peptide 2-Cyc. The
CC invention provides specific direct and targetted treatment of allergies
CC and related inflammatory conditions. The present sequence is Galphai2
CC peptide
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 57; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 1 KNNLKDCGLF 10

RESULT 5
ABJ36692
ID ABJ36692 standard; peptide; 11 AA.
XX
AC ABJ36692;
XX
DT 01-MAY-2003 (first entry)
XX
DE G protein coupled receptor related peptide SEQ ID No 17.
XX
KW Nootropic; cardiant; antiarteriosclerotic; hypotensive; cytostatic;
KW antibacterial; analgesic; antiallergic; antiasthmatic; antiinflammatory;
KW osteopathic; neuroprotective; anxiolytic; anorectic; lead compound;
KW G protein coupled receptor signaling inhibitor; GPCR; library;
KW high throughput screening assay; stroke; myocardial infarction;
KW restenosis; atherosclerosis; hypotension; cancer; infection; asthma;
KW septic shock; pain; allergic disorder; inflammatory bowel disease;
KW osteoporosis; obesity; psychotic; neurological disorder; anxiety;
KW schizophrenia; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN WO200272778-A2.
XX
PD 19-SEP-2002.
XX
PF 14-MAR-2002; 2002WO-US007561.
XX
PR 14-MAR-2001; 2001US-0275472P.
PR 11-MAY-2001; 2001US-00852910.
XX
PA (CUEB-) CUE BIOTECH.
XX
PI Gilchrist A, Hamm HE;
XX
DR WPI; 2003-247841/24.
XX
PT Identifying G protein coupled receptor (GPCR) signaling inhibitors,
PT useful in screening drugs for treating stroke, cancers or pain, by
PT identifying compounds that block GPCR mediated signaling with high
PT affinity and specificity.
XX
PS Claim 94; Page 24; 94pp; English.
XX
CC The invention relates to a novel method for identifying a G protein
CC coupled receptor (GPCR) signaling inhibitor. The novel method comprises
CC selecting or identifying a member of a library of peptides and/or
CC candidate compounds, having binding to a GPCR of higher affinity than
CC that of the native peptide. The peptide library is based on a native GPCR
CC binding peptide. The method is useful for identifying inhibitors of a G
CC protein coupled receptor (GPCR) signaling. The method is particularly
CC useful for identifying drugs that antagonise the binding between a GPCR
CC and its extracellular ligand(s). The method is especially useful in
CC modern high throughput screening assays for identifying potent lead
CC compounds. The compounds, peptides or inhibitors identified by the method
CC are useful for preventing, ameliorating or treating diseases in which
CC GPCR signaling is a causative factor or in which a specific class of G
CC protein is relevant, e.g. stroke, myocardial infarction, restenosis,
CC atherosclerosis, hypotension, cancers, infections, septic shock, pain,
CC allergic disorders, asthma, inflammatory bowel disease, osteoporosis,
CC obesity, or psychotic and neurological disorders (e.g. anxiety,
CC schizophrenia or Alzheimer's disease). This sequence represents a peptide
CC relating to the G protein coupled receptors of the invention
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 57; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 2 KNNLKDCGLF 11

RESULT 6
ABJ36771
ID ABJ36771 standard; peptide; 13 AA.
XX
AC ABJ36771;
XX
DT 01-MAY-2003 (first entry)
XX
DE G protein coupled receptor related peptide SEQ ID No 112.
XX
KW Nootropic; cardiant; antiarteriosclerotic; hypotensive; cytostatic;
KW antibacterial; analgesic; antiallergic; antiasthmatic; antiinflammatory;
KW osteopathic; neuroprotective; anxiolytic; anorectic; lead compound;
KW G protein coupled receptor signaling inhibitor; GPCR; library;
KW high throughput screening assay; stroke; myocardial infarction;
KW restenosis; atherosclerosis; hypotension; cancer; infection; asthma;
KW septic shock; pain; allergic disorder; inflammatory bowel disease;
KW osteoporosis; obesity; psychotic; neurological disorder; anxiety;
KW schizophrenia; Alzheimer's disease.
XX
OS Unidentified.
XX
PN WO200272778-A2.
XX
PD 19-SEP-2002.
XX
PF 14-MAR-2002; 2002WO-US007561.
XX
PR 14-MAR-2001; 2001US-0275472P.
PR 11-MAY-2001; 2001US-00852910.
XX
PA (CUEB-) CUE BIOTECH.
XX
PI Gilchrist A, Hamm HE;
XX
DR WPI; 2003-247841/24.
XX
PT Identifying G protein coupled receptor (GPCR) signaling inhibitors,

PT useful in screening drugs for treating stroke, cancers or pain, by
PT identifying compounds that block GPCR mediated signaling with high
PT affinity and specificity.
XX
PS Disclosure; Page 44; 94pp; English.
XX
CC The invention relates to a novel method for identifying a G protein
CC coupled receptor (GPCR) signaling inhibitor. The novel method comprises
CC selecting or identifying a member of a library of peptides and/or
CC candidate compounds, having binding to a GPCR of higher affinity than
CC that of the native peptide. The peptide library is based on a native GPCR
CC binding peptide. The method is useful for identifying inhibitors of a G
CC protein coupled receptor (GPCR) signaling. The method is particularly
CC useful for identifying drugs that antagonise the binding between a GPCR
CC and its extracellular ligand(s). The method is especially useful in
CC modern high throughput screening assays for identifying potent lead
CC compounds. The compounds, peptides or inhibitors identified by the method
CC are useful for preventing, ameliorating or treating diseases in which
CC GPCR signaling is a causative factor or in which a specific class of G
CC protein is relevant, e.g. stroke, myocardial infarction, restenosis,
CC atherosclerosis, hypotension, cancers, infections, septic shock, pain,
CC allergic disorders, asthma, inflammatory bowel disease, osteoporosis,
CC obesity, or psychotic and neurological disorders (e.g. anxiety,
CC schizophrenia or Alzheimer's disease). This sequence represents a peptide
CC relating to the G protein coupled receptors of the invention
XX
SQ Sequence 13 AA;

Query Match 100.0%; Score 57; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 4 KNNLKDCGLF 13

RESULT 7
ABW00010
ID ABW00010 standard; peptide; 13 AA.
XX
AC ABW00010;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human G alpha carboxy terminal peptide, Galphai1/2.
XX
KW G protein alpha; Galpha; myocardial infarction; atherosclerosis; therapy;
KW hypotension; hypertension; angina pectoris; stroke; Parkinson's disease;
KW Alzheimer's disease; rheumatoid arthritis; Grave's disease; diabetes;
KW obesity; cancer; infection; ulcer; human.
XX
OS Homo sapiens.
XX
PN US6559128-B1.
XX
PD 06-MAY-2003.
XX
PF 21-JAN-2000; 2000US-00489156.
XX
PR 21-JAN-2000; 2000US-00489156.
XX
PA (NOUN) UNIV NORTHWESTERN.
XX
PI Hamm HE, Gilchrist A;
XX
DR WPI; 2003-719631/68.
DR N-PSDB; AAD60735.
XX
PT New carboxy terminal G protein alpha (G alpha) peptides which block G
PT protein signaling, useful for treating pathological disorders such as
PT stroke, myocardial infarction, atherosclerosis, hypotension, and
PT hypertension.
XX
PS Claim 2; Fig 2B; 43pp; English.
XX
CC The present invention relates to new carboxy terminal G protein alpha
CC (Galpha) peptides which block G protein signalling. The invention is
CC useful for treating pathological diseases such as stroke, myocardial
CC infarction, atherosclerosis, hypotension, hypertension, angina pectoris,
CC cancers, bacterial infections, fungal infections, viral infections,
CC rheumatoid arthritis, Grave's disease, diabetes, obesity, ulcer,
CC Parkinson's disease, Alzheimer's disease. The invention is also useful
CC for preventing conception in a mammal. The present sequence is human G
CC alpha carboxy terminal peptide
XX
SQ Sequence 13 AA;

Query Match 100.0%; Score 57; DB 7; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 4 KNNLKDCGLF 13

RESULT 8
ADF45264
ID ADF45264 standard; peptide; 13 AA.
XX
AC ADF45264;
XX
DT 12-FEB-2004 (first entry)
XX
DE G alpha carboxy terminal peptide #2.
XX
KW minigene; modified carboxy terminal alpha peptide; G-protein;
KW G-protein coupled receptor; GPCR; G-protein-mediated signaling event;
KW stroke; myocardial infarction; restenosis; atherosclerosis; hypotension;
KW hypertension; angina pectoris; cancer; bacterial infection;
KW fungal infection; protozoan infection; viral infection; septic shock;
KW pain; chronic allergic disorder; asthma; inflammatory bowel disease;
KW osteoporosis; rheumatoid arthritis; Grave's disease; diabetes;
KW vascular sclerosis; chronic rejection; urinary retention; infertility;
KW ulcer; obesity; benign prostatic hypertrophy; anxiety; epilepsy;
KW schizophrenia; manic depression; Parkinson's disease;
KW Alzheimer's disease; delirium; dementia; drug addiction,; anorexia;
KW bulimia.
XX
OS Synthetic.
XX
PN US2003162258-A1.
XX
PD 28-AUG-2003.
XX
PF 24-FEB-2003; 2003US-00373540.
XX
PR 21-JAN-2000; 2000US-00489156.
XX
PA (NOUN) UNIV NORTHWESTERN.
XX
PI Hamm HE, Gilchrist A;
XX
DR WPI; 2003-897929/82.
DR N-PSDB; ADF45298.
XX
PT New nucleic acid molecule comprising a minigene that encodes a modified
PT carboxy terminal Galpha peptide, useful for blocking G-protein-mediated
PT signaling events or for treating disorders such as stroke, cancer or
PT atherosclerosis.
XX
PS Claim 10; SEQ ID NO 16; 47pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising a minigene,
CC where the minigene encodes a modified carboxy terminal alpha peptide that

```
CC   blocks the site of interaction between a G-protein and a G-protein
CC   coupled receptor (GPCR) in a cell. The composition and methods are useful
CC   in blocking G-protein-mediated signaling events. These may also be used
CC   for identifying unknown interactions between G-proteins and GPCRs, and
CC   for treating pathological disorders associated with G-protein-mediated
CC   signaling events, such as stroke, myocardial infarction, restenosis,
CC   atherosclerosis, hypotension, hypertension, angina pectoris, cancers,
CC   bacterial infections, fungal infections, protozoan infections, viral
CC   infections, septic shock, pain, chronic allergic disorders, asthma,
CC   inflammatory bowel disease, osteoporosis, rheumatoid arthritis, Grave's
CC   disease, diabetes, disorders associated with solid organ transplant,
CC   vascular sclerosis, chronic rejection, urinary retention, infertility,
CC   ulcers, obesity, benign prostatic hypertrophy, anxiety, epilepsy,
CC   schizophrenia, manic depression, Parkinson's disease, Alzheimer's
CC   disease, delirium, dementia, drug addiction, anorexia or bulimia. The
CC   present sequence is used in the exemplification of the invention.
XX
SQ   Sequence 13 AA;

  Query Match             100.0%;  Score 57;  DB 7;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 0.0017;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db          4 KNNLKDCGLF 13


RESULT 9
AAO08372
ID   AAO08372 standard; protein; 23 AA.
XX
AC   AAO08372;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human polypeptide SEQ ID NO 22264.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW   vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW   tissue growth factor; immunomodulatory; cancer; leukaemia;
KW   nervous system disorders; arthritis; inflammation.
XX
OS   Homo sapiens.
XX
PN   WO200164835-A2.
XX
PD   07-SEP-2001.
XX
PF   26-FEB-2001; 2001WO-US004927.
XX
PR   28-FEB-2000; 2000US-00515126.
PR   18-MAY-2000; 2000US-00577409.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT;
XX
DR   WPI; 2001-514838/56.
DR   N-PSDB; AAI88303.
XX
PT   Isolated nucleic acids and polypeptides, useful for preventing diagnosing
PT   and treating e.g. leukemia, inflammation and immune disorders.
XX
PS   Claim 20; SEQ ID NO 22264; 1399pp + Sequence Listing; English.
XX
CC   The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC   the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC   cytokine, cell proliferation or cell differentiation or which may induce
CC   production of other cytokines in other cell populations. The
CC   polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC   peptide therapy. The polypeptides have various cytokine-like activities,
CC   e.g. stem cell growth factor activity, haematopoiesis regulating
CC   activity, tissue growth factor activity, immunomodulatory activity and
CC   activin/inhibin activity and may be useful in the diagnosis and/or
CC   treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC   inflammation. Note: The sequence data for this patent did not form part
CC   of the printed specification, but was obtained in electronic format
CC   directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 23 AA;

  Query Match             100.0%;  Score 57;  DB 4;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 0.0031;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db         14 KNNLKDCGLF 23


RESULT 10
AAY72144
ID   AAY72144 standard; peptide; 26 AA.
XX
AC   AAY72144;
XX
DT   24-APR-2001  (first entry)
XX
DE   Modified anti-allergic peptide 5m.
XX
KW   Anti-allergic peptide; therapeutic; migraine; psoriasis; asthma;
KW   multiple sclerosis; nasal allergy; mast cell degranulation; histamine;
KW   allergy; eye; skin; acute urticaria; interstitial cystitis; vasotropic;
KW   psychogenic; bowel disease; dermatological; antiinflammatory; G alphat;
KW   neuroprotective; antipsoriatic; Kaposi fibroblast growth factor;
KW   fusion peptide.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .16
FT                   /label= Signal_peptide
FT                   /note= "Signal sequence of Kaposi fibroblast growth
FT                   factor; this region is referred in claim 48"
FT   Peptide         17. .26
FT                   /label= G_alphat_peptide
FT                   /note= "Corresponds to C-terminal sequence of G alphat"
FT   Misc-difference 18
FT                   /note= "Wild type Glu substituted with Asn"
XX
PN   WO200078346-A1.
XX
PD   28-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-IL000346.
XX
PR   17-JUN-1999;   99IL-00130526.
XX
PA   (ALLE-) ALLERGENE LTD.
XX
PI   Eisenberg R,  Raz T;
XX
DR   WPI; 2001-080758/09.
XX
PT   Novel anti-allergic agents for treating allergic conditions such as
PT   allergic reactions in eye, skin, nasal allergy, asthma, migraines, has
PT   peptides for cell penetration and reducing mast cell degranulation.
XX
PS   Example 2; Page 20; 63pp; English.
XX
CC   The present sequence is modified anti-allergic peptide 5m consisting of a
CC   signal sequence of Kaposi fibroblast growth factor, linked to the C-
CC   terminal G alphat sequence. The last 10 amino acids of this peptide are
CC   homologous to the C-terminal G alphai2 sequence. The invention relates to
CC   therapeutic complex molecules which are useful as anti-allergic agents.
```

CC These anti-allergic agents are useful for treating allergic conditions
CC such as nasal allergy, allergic reaction in the eye or skin, acute
CC urticaria, psoriasis, psychogenic or allergic asthma, interstitial
CC cystitis, bowel diseases, migraines and multiple sclerosis. The
CC therapeutic complex is highly specific, direct and provides targetted
CC treatment of allergies and related inflammatory conditions. It comprises
CC molecules having at least a first segment ie., a signal peptide which is
CC competent for the importation of the complex into the mast cells, and a
CC second segment which is having the anti-allergic effect is able to block
CC or significantly reduce the G protein-mediated contribution to mast cell
CC degranulation and in turn the release of histamine. The invention also
CC discloses methods for preventing and treating allergies
XX
SQ Sequence 26 AA;

Query Match 100.0%; Score 57; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 17 KNNLKDCGLF 26

RESULT 11
AAY72145
ID AAY72145 standard; peptide; 27 AA.
XX
AC AAY72145;
XX
DT 24-APR-2001 (first entry)
XX
DE Anti-allergic peptide 12.
XX
KW Anti-allergic peptide; therapeutic; migraine; psoriasis; asthma;
KW multiple sclerosis; nasal allergy; mast cell degranulation; histamine;
KW allergy; eye; skin; acute urticaria; interstitial cystitis; vasotropic;
KW psychogenic; bowel disease; dermatological; antiinflammatory; G alphat;
KW neuroprotective; antipsoriatic; Kaposi fibroblast growth factor;
KW fusion peptide.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 2. .17
FT /label= Signal_peptide
FT /note= "Signal sequence of Kaposi fibroblast growth
FT factor; this region is referred in claim 48"
FT Peptide 18. .27
FT /label= G_alphat_peptide
FT /note= "Corresponds to C-terminal sequence of G alphat"
FT Misc-difference 19
FT /note= "Wild type Glu substituted with Asn"
XX
PN WO200078346-A1.
XX
PD 28-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-IL000346.
XX
PR 17-JUN-1999; 99IL-00130526.
XX
PA (ALLE-) ALLERGENE LTD.
XX
PI Eisenberg R, Raz T;
XX
DR WPI; 2001-080758/09.
XX
PT Novel anti-allergic agents for treating allergic conditions such as
PT allergic reactions in eye, skin, nasal allergy, asthma, migraines, has
PT peptides for cell penetration and reducing mast cell degranulation.
XX
PS Example 2; Page 20; 63pp; English.

XX
CC The present sequence is anti-allergic peptide 12 consisting of a signal
CC sequence of Kaposi fibroblast growth factor, linked to the C-terminal G
CC alphat sequence. This peptide is obtained by adding a lysine residue to
CC the N-terminus of anti-allergic peptide 5 (AAY72142), for improving the
CC peptide solubility. The invention relates to therapeutic complex
CC molecules which are useful as anti-allergic agents. These anti-allergic
CC agents are useful for treating allergic conditions such as nasal allergy,
CC allergic reaction in the eye or skin, acute urticaria, psoriasis,
CC psychogenic or allergic asthma, interstitial cystitis, bowel diseases,
CC migraines and multiple sclerosis. The therapeutic complex is highly
CC specific, direct and provides targetted treatment of allergies and
CC related inflammatory conditions. It comprises molecules having at least a
CC first segment ie., a signal peptide which is competent for the
CC importation of the complex into the mast cells, and a second segment
CC which is having the anti-allergic effect is able to block or
CC significantly reduce the G protein-mediated contribution to mast cell
CC degranulation and in turn the release of histamine. The invention also
CC discloses methods for preventing and treating allergies
XX
SQ Sequence 27 AA;

Query Match 100.0%; Score 57; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 18 KNNLKDCGLF 27

RESULT 12
ABR41313
ID ABR41313 standard; protein; 288 AA.
XX
AC ABR41313;
XX
DT 02-JUN-2003 (first entry)
XX
DE Human DITHP intracellular signalling protein.
XX
KW Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;
KW cancer; cell proliferative disorder; autoimmune disorder;
KW inflammatory disorder; infection; hormonal disorder; metabolic disorder;
KW neurological disorder; gastrointestinal disorder; transport disorder;
KW connective tissue disorder; drug screening; proteome analysis;
KW gene therapy; antisense therapy; genotyping; transgenic animal; knock in;
KW disease model; toxicological testing; transcript imaging;
KW intracellular signalling.
XX
OS Homo sapiens.
XX
PN WO200297031-A2.
XX
PD 05-DEC-2002.
XX
PF 27-MAR-2002; 2002WO-US010056.
XX
PR 28-MAR-2001; 2001US-0279619P.
PR 29-MAR-2001; 2001US-0280067P.
PR 29-MAR-2001; 2001US-0280068P.
PR 16-MAY-2001; 2001US-0291280P.
PR 17-MAY-2001; 2001US-0291829P.
PR 17-MAY-2001; 2001US-0291849P.
PR 19-JUN-2001; 2001US-0299428P.
PR 20-JUN-2001; 2001US-0299776P.
PR 20-JUN-2001; 2001US-0300001P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
PI Daughtery SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;

PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
XX
DR WPI; 2003-129518/12.
DR N-PSDB; ACC46254.
XX
PT Novel human diagnostic and therapeutic polypeptide useful for identifying
PT test compound which specifically binds to a polypeptide encoded by human
PT diagnostic and therapeutic polynucleotide, and to induce antibodies.
XX
PS Claim 27; SEQ ID NO 848; 591pp; English.
XX
CC The invention relates to novel human diagnostic and therapeutic
CC polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded
CC proteins (DITHP; ABR41136-ABR41812). The invention also relates to
CC polynucleotide sequences at least 90% identical to the dithp cDNA
CC sequences of the invention; recombinant vectors, host cells and
CC transgenic organisms comprising a dithp nucleic acid sequence; the
CC recombinant production of DITHP proteins; antibodies specific for DITHP
CC proteins; microarrays comprising dithp nucleic acid sequences; methods of
CC detecting dithp nucleotide and protein sequences; methods of screening
CC for compounds which specifically bind a DITHP protein; and methods of
CC assessing the toxicity of test compounds using a dithp hybridisation
CC probe. Dithp nucleic acid sequences and DITHP proteins may be used in the
CC diagnosis of a wide variety of conditions including cancer and other cell
CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,
CC viral, fungal or parasitic infections; hormonal disorders; metabolic
CC disorders; neurological disorders; gastrointestinal disorders; transport
CC disorders; and connective tissue disorders. They may also be used to
CC screen for modulators of protein activity or gene expression. DITHP
CC proteins can additionally be used in analysis of the proteome of a tissue
CC or cell type and to induce antibodies. The dithp nucleic acids are
CC additionally useful in somatic or germline gene therapy of the disorders
CC mentioned above, as a source of antisense sequences, as a source of
CC probes and primers, in genotyping and identification of individuals, in
CC the generation of transgenic animal models of human disease or knock in
CC humanised animals, in toxicological testing, and in transcript imaging.
CC The present sequence represents a DITHP protein which has intracellular
CC signalling activity. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 288 AA;

Query Match 100.0%; Score 57; DB 6; Length 288;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 279 KNNLKDCGLF 288

RESULT 13
ADM05136
ID ADM05136 standard; protein; 339 AA.
XX
AC ADM05136;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human protein of the invention SEQ ID NO:3821.
XX
KW human; gene therapy; diagnostic marker; pharmaceutical.
XX
OS Homo sapiens.
XX
PN EP1347046-A1.
XX
PD 24-SEP-2003.
XX
PF 12-APR-2002; 2002EP-00008400.
XX
PR 22-MAR-2002; 2002JP-00137785.
XX
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
DR WPI; 2003-723558/69.
DR N-PSDB; ADM02693.
XX
PT New polynucleotides and polypeptides are useful in gene therapy, for
PT developing a diagnostic marker or medicines for regulating their
PT expression and activity, or as a target of gene therapy.
XX
PS Claim 1; SEQ ID NO 3821; 305pp; English.
XX
CC The invention relates to a novel human polynucleotide and the encoded
CC polypeptide. A polynucleotide of the invention may have a use in gene
CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
CC as a primer for synthesizing the polynucleotide or as a probe for
CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
CC useful in gene therapy, for developing a diagnostic marker or medicines
CC for regulating their expression and activity, or as a target of gene
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
CC are useful as pharmaceutical agents. The present sequence represents a
CC protein sequence of the invention.
XX
SQ Sequence 339 AA;

Query Match 100.0%; Score 57; DB 7; Length 339;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 330 KNNLKDCGLF 339

RESULT 14
ADM04957
ID ADM04957 standard; protein; 339 AA.
XX
AC ADM04957;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human protein of the invention SEQ ID NO:3642.
XX
KW human; gene therapy; diagnostic marker; pharmaceutical.
XX
OS Homo sapiens.
XX
PN EP1347046-A1.
XX
PD 24-SEP-2003.
XX
PF 12-APR-2002; 2002EP-00008400.
XX
PR 22-MAR-2002; 2002JP-00137785.
XX
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
DR WPI; 2003-723558/69.
DR N-PSDB; ADM02514.
XX
PT New polynucleotides and polypeptides are useful in gene therapy, for
PT developing a diagnostic marker or medicines for regulating their
PT expression and activity, or as a target of gene therapy.

XX
PS Claim 1; SEQ ID NO 3642; 305pp; English.
XX
CC The invention relates to a novel human polynucleotide and the encoded
CC polypeptide. A polynucleotide of the invention may have a use in gene
CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
CC as a primer for synthesizing the polynucleotide or as a probe for
CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
CC useful in gene therapy, for developing a diagnostic marker or medicines
CC for regulating their expression and activity, or as a target of gene
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
CC are useful as pharmaceutical agents. The present sequence represents a
CC protein sequence of the invention.
XX
SQ Sequence 339 AA;

Query Match 100.0%; Score 57; DB 7; Length 339;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 330 KNNLKDCGLF 339

RESULT 15
ADE57521
ID ADE57521 standard; protein; 353 AA.
XX
AC ADE57521;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein P04898, SEQ ID NO 3383.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; P04898.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 353 AA;

Query Match 100.0%; Score 57; DB 7; Length 353;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 344 KNNLKDCGLF 353

RESULT 16
ADE57515
ID ADE57515 standard; protein; 353 AA.
XX
AC ADE57515;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein P10824, SEQ ID NO 3377.
XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; P10824.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence

```
CC   which is differentially regulated in an animal subjected to pain and a
CC   kit to perform the method, an array, a method for identifying an agent
CC   that increases or decreases the expression of the polynucleotide sequence
CC   that is differentially expressed in neuronal tissue of a first animal
CC   subjected to pain, a method for identifying a compound which regulates
CC   the expression of a polynucleotide sequence which is differentially
CC   expressed in an animal subjected to pain, a method for identifying a
CC   compound that regulates the activity of one or more of the
CC   polynucleotides, a method for producing a pharmaceutical composition, a
CC   method for identifying a compound or small molecule that regulates the
CC   activity in an animal of one or more of the polypeptides given in the
CC   specification, a method for identifying a compound useful in treating
CC   pain and a pharmaceutical composition comprising the one or more
CC   polypeptides or their antibodies. The polynucleotide or the compound that
CC   modulates its activity is useful for preparing a medicament for treating
CC   pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC   injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC   therapy). The sequence presented is a rat protein (shown in Table 2 of
CC   the specification) which is differentially expressed during pain. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic form directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 353 AA;

  Query Match             100.0%;  Score 57;  DB 7;  Length 353;
  Best Local Similarity   100.0%;  Pred. No. 0.06;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        344 KNNLKDCGLF 353


RESULT 17
ADE57517
ID   ADE57517 standard; protein; 353 AA.
XX
AC   ADE57517;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human Protein P04898, SEQ ID NO 3379.
XX
KW   Human; pain; neuronal tissue; gene therapy;
KW   spinal segmental nerve injury; chronic constriction injury; CCI;
KW   spared nerve injury; SNI; Chung.
XX
OS   Homo sapiens.
XX
PN   WO2003016475-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US025765.
XX
PR   14-AUG-2001; 2001US-0312147P.
PR   01-NOV-2001; 2001US-0346382P.
PR   26-NOV-2001; 2001US-0333347P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
XX
PI   Woolf C,  D'urso D,  Befort K,  Costigan M;
XX
DR   WPI; 2003-268312/26.
DR   GENBANK; P04898.
XX
PT   New composition comprising two or more isolated polypeptides, useful for
PT   preparing a medicament for treating pain in an animal.
XX
PS   Claim 1; Page; 1017pp; English.
XX
CC   The invention discloses a composition comprising two or more isolated rat
CC   or human polynucleotides or a polynucleotide which represents a fragment,
CC   derivative or allelic variation of the nucleic acid sequence. Also
CC   claimed are a vector comprising the novel polynucleotide, a host cell
CC   comprising the vector, a method for identifying a nucleotide sequence
CC   which is differentially regulated in an animal subjected to pain and a
CC   kit to perform the method, an array, a method for identifying an agent
CC   that increases or decreases the expression of the polynucleotide sequence
CC   that is differentially expressed in neuronal tissue of a first animal
CC   subjected to pain, a method for identifying a compound which regulates
CC   the expression of a polynucleotide sequence which is differentially
CC   expressed in an animal subjected to pain, a method for identifying a
CC   compound that regulates the activity of one or more of the
CC   polynucleotides, a method for producing a pharmaceutical composition, a
CC   method for identifying a compound or small molecule that regulates the
CC   activity in an animal of one or more of the polypeptides given in the
CC   specification, a method for identifying a compound useful in treating
CC   pain and a pharmaceutical composition comprising the one or more
CC   polypeptides or their antibodies. The polynucleotide or the compound that
CC   modulates its activity is useful for preparing a medicament for treating
CC   pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC   injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC   therapy). The sequence presented is a human protein (shown in Table 2 of
CC   the specification) which is differentially expressed during pain. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic form directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 353 AA;

  Query Match             100.0%;  Score 57;  DB 7;  Length 353;
  Best Local Similarity   100.0%;  Pred. No. 0.06;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        344 KNNLKDCGLF 353


RESULT 18
ADE57519
ID   ADE57519 standard; protein; 353 AA.
XX
AC   ADE57519;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Rat Protein P10824, SEQ ID NO 3381.
XX
KW   Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW   chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS   Rattus norvegicus.
XX
PN   WO2003016475-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US025765.
XX
PR   14-AUG-2001; 2001US-0312147P.
PR   01-NOV-2001; 2001US-0346382P.
PR   26-NOV-2001; 2001US-0333347P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
XX
PI   Woolf C,  D'urso D,  Befort K,  Costigan M;
XX
DR   WPI; 2003-268312/26.
DR   GENBANK; P10824.
XX
PT   New composition comprising two or more isolated polypeptides, useful for
```

PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 353 AA;

Query Match 100.0%; Score 57; DB 7; Length 353;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 344 KNNLKDCGLF 353

RESULT 19
ADN06152
ID ADN06152 standard; protein; 353 AA.
XX
AC ADN06152;
XX
DT 01-JUL-2004 (first entry)
XX
DE Rat Gi1-Human Gq chimeric alpha subunit (Gi1q31N25C).
XX
KW G protein; alpha subunit; physiological response; neurotransmitter;
KW sensory stimuli; rat; Gi1 alpha subunit; human; Gq.
XX
OS Rattus sp.
OS Homo sapiens.
OS Chimeric.
XX
PN US2004072157-A1.
XX
PD 15-APR-2004.
XX
PF 31-JAN-2002; 2002US-00059266.
XX
PR 31-JAN-2001; 2001US-0265068P.
XX
PA (GRAB/) GRABER S G.
XX
PI Graber SG;
XX
DR WPI; 2004-328563/30.
DR N-PSDB; ADN06151.
XX
PT New chimeric approximatelya subunit of G proteins that affect receptor
PT coupling of the G proteins, useful in mediating an array of physiological
PT responses initiated by hormones, neurotransmitters and sensory stimuli.
XX
PS Claim 19; SEQ ID NO 18; 68pp; English.
XX
CC The invention relates to chimeric alpha subunit of G proteins. The
CC chimeric alpha subunit of G proteins is useful in mediating an array of
CC physiological responses initiated by hormones, neurotransmitters, sensory
CC stimuli and other signalling molecules. The present sequence is rat Gi1-
CC human Gq chimeric alpha subunit protein.
XX
SQ Sequence 353 AA;

Query Match 100.0%; Score 57; DB 8; Length 353;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 344 KNNLKDCGLF 353

RESULT 20
AAY85290
ID AAY85290 standard; protein; 354 AA.
XX
AC AAY85290;
XX
DT 14-JUL-2000 (first entry)
XX
DE Human G-alpha-i1 amino acid sequence.
XX
KW G-alpha-i1; G protein; adenylyl cyclase hormonal inhibition; tumour;
KW plasma membrane regulation; antisense composition; treatment; prevent;
KW delay; infection; inflammation; tumour formation; research; diagnose.
XX
OS Homo sapiens.
XX
PN US6046321-A.
XX
PD 04-APR-2000.
XX
PF 09-APR-1999; 99US-00289377.
XX
PR 09-APR-1999; 99US-00289377.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cowsert LM;
XX
DR WPI; 2000-292434/25.
DR N-PSDB; AAA10854.
XX
PT New antisense compounds targeting nucleic acids encoding human G-alpha-i1
PT useful for modulating G-alpha-i1 expression and for treating diseases
PT associated with G-alpha-i1 expression.
XX
PS Disclosure; Col 41-44; 31pp; English.
XX
CC This sequence represents the human G-alpha-i1 amino acid sequence. Human
CC G-alpha-i1 is a member of the Gi subfamily of G proteins which is
CC involved in hormonal inhibition of adenylyl cyclase and in the regulation
CC of plasma membrane enzymes. The expression of G-alpha-i1 is altered in
CC some tumours. The invention relates to antisense oligonucleotides
CC represented in AAA10814-A10853 which inhibit the expression of G-alpha-
CC i1. The antisense oligonucleotides can be used in the treatment of
CC diseases or conditions associated with the expression of G-alpha-i1 by
CC modulating the expression of G-alpha-i1 in cells or tissues. The
CC antisense compositions may also be used prophylactically, e.g. to prevent
CC or delay infection, inflammation, or tumour formation. Furthermore, the

CC antisense oligonucleotides may also be useful in research and
CC diagnostics, e.g. in detecting nucleic acids encoding G-alpha-i1 by
CC conjugation of an enzyme to the oligonucleotide, or radiolabelling the
CC oligonucleotide. Kits using such detection means for detecting the level
CC of G-alpha-i1 in the sample may also be prepared. Antisense
CC oligonucleotides, which are able to inhibit specific gene expression, are
CC often used to elucidate the function of particular genes. These antisense
CC compounds are also used to distinguish between functions of various
CC members of a biological pathway
XX
SQ Sequence 354 AA;

Query Match 100.0%; Score 57; DB 3; Length 354;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 345 KNNLKDCGLF 354

RESULT 21
AAB99064
ID AAB99064 standard; protein; 354 AA.
XX
AC AAB99064;
XX
DT 23-AUG-2001 (first entry)
XX
DE Human G-protein alpha subunit i1.
XX
KW G-protein coupled receptor; GPCR; GnRH receptor; disease treatment;
KW gonadotrophin releasing; hormone receptor; hormone dependent cancer;
KW human; catfish; goldfish; cow; sheep; horse; fruitfly; pig; rat; mouse;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN WO200136446-A2.
XX
PD 25-MAY-2001.
XX
PF 17-NOV-2000; 2000WO-GB004385.
XX
PR 17-NOV-1999; 99GB-00027215.
XX
PA (UYBR-) UNIV BRISTOL.
XX
PI Mcardle CA;
XX
DR WPI; 2001-355607/37.
XX
PT Use of a vector encoding G-protein coupled receptors for manufacturing
PT medicaments for treating cancer, diseases of cardiovascular system,
PT nervous system, digestive system, immune system, or muscle diseases.
XX
PS Disclosure; Fig 19; 78pp; English.
XX
CC The present invention describes a prodrug comprising a vector encoding a
CC G-protein coupled receptor (GPCR). This can be used in the treatment of
CC diseases, including hormone-dependent cancers, cardiovascular, nervous
CC system, digestive system, immune system, respiratory, skeletal,
CC endocrine, sensory and muscle diseases and disorders. The present
CC sequence is a protein described in the exemplification of the invention
XX
SQ Sequence 354 AA;

Query Match 100.0%; Score 57; DB 4; Length 354;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 345 KNNLKDCGLF 354

RESULT 22
ABB09273
ID ABB09273 standard; protein; 354 AA.
XX
AC ABB09273;
XX
DT 10-JUL-2002 (first entry)
XX
DE G protein-coupled receptor (GPCR) I1 SEQ ID NO:19.
XX
KW Target activated nucleic acid biosensor; signalling moiety; GPCR;
KW nucleic acid sensor; detection; engineering; drug optimisation;
KW G protein-coupled receptor.
XX
OS Homo sapiens.
XX
PN WO200222882-A2.
XX
PD 21-MAR-2002.
XX
PF 13-SEP-2001; 2001WO-US028835.
XX
PR 13-SEP-2000; 2000US-0232454P.
XX
PA (ARCH-) ARCHEMIX CORP.
XX
PI Stanton M, Epstein D, Hamaguchi N;
XX
DR WPI; 2002-393977/42.
XX
PT Nucleic acid sensor for detecting target molecule, comprises target
PT molecule activation site and optical signaling unit that changes its
PT optical properties upon allosteric modulation sensor after recognition of
PT target.
XX
PS Example 12; Page 89; 144pp; English.
XX
CC The present invention describes a nucleic acid sensor molecule (I)
CC comprising a target molecule activation site comprising a structure that
CC recognises a target molecule and an optical signalling unit including at
CC least one nucleotide coupled to a signalling moiety that changes its
CC optical properties upon allosteric modulation of (I) following
CC recognition of the target molecule. (I) is useful for detecting a target
CC molecule associated with a pathological condition or genetic alteration.
CC (I) is useful for identifying a drug compound, by identifying a nucleic
CC acid biosensor-based molecule profile of target molecules associated with
CC a disease trait in a patient, administering a candidate compound to the
CC patient, and monitoring changes in the profile. Alternately, the method
CC involves identifying a number of pathway target molecules, administering
CC a candidate compound to a patient having a disease trait, and monitoring
CC changes in the structure, level or activity of two or more of the pathway
CC target molecules using (I). The profile of target molecules or the
CC changes in the structure is compared to the profile of a reference
CC healthy or diseased population. (I) is useful in multiple assays, for the
CC detection of target molecule. (I) is also useful in diagnostic
CC applications and drug optimisation. The present sequence represents a G
CC protein-coupled receptor, which is used in an example from the present
CC invention
XX
SQ Sequence 354 AA;

Query Match 100.0%; Score 57; DB 5; Length 354;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 345 KNNLKDCGLF 354

```
RESULT 23
ABR82632
ID   ABR82632 standard; protein; 354 AA.
XX
AC   ABR82632;
XX
DT   04-DEC-2003  (first entry)
XX
DE   C. elegans EGL-30 protein related fragment G(i).
XX
KW   RGS; G-protein; regulator of G-protein signaling; Galphaq; uropathic;
KW   antidepressant; tranquillizer; antiarrhythmic; relaxant; EGL-30;
KW   nematode.
XX
OS   Caenorhabditis elegans.
XX
PN   WO2003063784-A2.
XX
PD   07-AUG-2003.
XX
PF   28-JAN-2003; 2003WO-US002452.
XX
PR   28-JAN-2002; 2002US-0352720P.
XX
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
PA   (EXEL-) EXELIXIS INC.
XX
PI   Moore L,  Kindt RM,  Kopczynski J,  Doberstein SK,  Cockett M;
PI   Ramanathan C,  Lodge N,  Fitzgerald K,  Stouch T;
XX
DR   WPI; 2003-646090/61.
XX
PT   Screening agents that modulate interaction of regulator of G-protein
PT   signaling and Galphaq, comprises contacting one of the proteins with a
PT   candidate agent in an assay system and detecting the candidate agent-
PT   biased activity of the system.
XX
PS   Example 5; Fig 1B; 105pp; English.
XX
CC   The invention relates to screening agents that modulate the interaction
CC   of regulator of G-protein signaling (RGS) and Galphaq proteins. The
CC   method involves (a) contacting a screening assay system comprising a RGS
CC   or Galphaq polypeptide, with an agent; and (b) detecting an agent-biased
CC   activity of the system, where a difference between the agent-biased and
CC   reference activity indicates the modulatory action of the agent on RGS
CC   and Galphaq interaction. The method is useful for identifying agents that
CC   modulate urinary incontinence. The modulators are useful for treating or
CC   preventing urinary incontinence, depression, anxiety, arrhythmia,
CC   cognitive disorders, psychosis, skeletal muscle disorders, cardiac muscle
CC   disorders, smooth muscle disorders, muscle spasms, skeletal muscle
CC   spasms, cardiac muscle spasms, smooth muscle spasms, muscle contraction
CC   disorders, and muscle relaxation disorders. Sequences ABR82630-637
CC   represent C. elegans Gaq homologue, EGL-30 protein and related fragments
XX
SQ   Sequence 354 AA;

  Query Match             100.0%;  Score 57;  DB 7;  Length 354;
  Best Local Similarity   100.0%;  Pred. No. 0.06;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        345 KNNLKDCGLF 354


RESULT 24
ADC09608
ID   ADC09608 standard; protein; 354 AA.
XX
AC   ADC09608;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human G-protein coupled receptor-related protein, SEQ ID 19.
XX
KW   Nucleic acid sensor molecule; ligase; cis-hammerhead; protein kinase;
KW   human; G-protein coupled receptor.
XX
OS   Homo sapiens.
XX
PN   WO2003014375-A2.
XX
PD   20-FEB-2003.
XX
PF   09-AUG-2002; 2002WO-US025319.
XX
PR   09-AUG-2001; 2001US-0311378P.
PR   21-AUG-2001; 2001US-0313932P.
PR   13-SEP-2001; 2001US-00952680.
PR   13-NOV-2001; 2001US-0338186P.
PR   18-JAN-2002; 2002US-0349959P.
PR   13-MAR-2002; 2002US-0364486P.
PR   25-MAR-2002; 2002US-0367991P.
PR   04-APR-2002; 2002US-0369887P.
PR   01-MAY-2002; 2002US-0376744P.
PR   31-MAY-2002; 2002US-0385097P.
XX
PA   (ARCH-) ARCHEMIX CORP.
XX
PI   Stanton M,  Epstein D,  Hamaguchi N,  Kurz M,  Keefe T,  Wilson C;
PI   Grate D,  Marshall KA,  Mccauley T,  Kurz J;
XX
DR   WPI; 2003-300534/29.
XX
PT   Nucleic acid sensor molecule, for identifying/detecting protein kinase in
PT   a sample, comprises a target modulation domain which recognizes a target
PT   molecule, a linker domain, a catalytic domain, and an optical signal
PT   generator.
XX
PS   Example 5; SEQ ID NO 19; 423pp; English.
XX
CC   The present invention relates to nucleic acid sensor molecules (I), which
CC   comprise a target modulation domain that recognizes a target molecule
CC   (TM), a linker domain, a catalytic domain, and an optical signal
CC   generating unit. The catalytic domain comprises a ligase or cis-
CC   hammerhead. (I) are useful for identifying or detecting TM in a sample,
CC   preferably a protein kinase in a sample. Target molecules include
CC   proteins, post-translationally modified forms of proteins, peptides,
CC   nucleic acids, oligosaccharides, nucleotides, metabolites, drugs, toxins,
CC   biohazards, ions, carbohydrates, polysaccharides, hormones, receptors,
CC   antigens, antibodies, viruses, metabolites, co-factors, drugs, dyes,
CC   nutrients, growth factors, cCMP, cAMP or cGMP, protein kinase,
CC   phosphorylated protein kinase, extracellular signal regulated kinase
CC   (ERK), a component or product of mitogen activated protein (MAP) kinase
CC   pathway, a MAP kinase pathway associated protein, an extracellular
CC   component of MAP kinase pathway, a component of ERK1/2 MAP, JNK MAP or
CC   P38 MAP kinase pathway, an endogenous form of MAP kinase (MEK), MAP
CC   kinase kinase, or MAP kinase (MEKKK), or RAF kinase, Ras protein,
CC   phosphatase, GTP binding protein, G-protein coupled receptor (GPCR),
CC   cytokine, growth factor, cellular metabolite, small molecule or lysozyme.
CC   (I) are also useful for identifying a modulator of protein kinase
CC   activity. In an example from the invention, nucleic acid sensor molecules
CC   which signal human G-protein coupled receptors e.g. the present sequence,
CC   were obtained.
XX
SQ   Sequence 354 AA;

  Query Match             100.0%;  Score 57;  DB 7;  Length 354;
  Best Local Similarity   100.0%;  Pred. No. 0.06;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        345 KNNLKDCGLF 354
```

```
RESULT 25
ADE59387
ID   ADE59387 standard; protein; 354 AA.
XX
AC   ADE59387;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human Protein P04899, SEQ ID NO 5281.
XX
KW   Human; pain; neuronal tissue; gene therapy;
KW   spinal segmental nerve injury; chronic constriction injury; CCI;
KW   spared nerve injury; SNI; Chung.
XX
OS   Homo sapiens.
XX
PN   WO2003016475-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US025765.
XX
PR   14-AUG-2001; 2001US-0312147P.
PR   01-NOV-2001; 2001US-0346382P.
PR   26-NOV-2001; 2001US-0333347P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
XX
PI   Woolf C,  D'urso D,  Befort K,  Costigan M;
XX
DR   WPI; 2003-268312/26.
DR   GENBANK; P04899.
XX
PT   New composition comprising two or more isolated polypeptides, useful for
PT   preparing a medicament for treating pain in an animal.
XX
PS   Claim 1; Page; 1017pp; English.
XX
CC   The invention discloses a composition comprising two or more isolated rat
CC   or human polynucleotides or a polynucleotide which represents a fragment,
CC   derivative or allelic variation of the nucleic acid sequence. Also
CC   claimed are a vector comprising the novel polynucleotide, a host cell
CC   comprising the vector, a method for identifying a nucleotide sequence
CC   which is differentially regulated in an animal subjected to pain and a
CC   kit to perform the method, an array, a method for identifying an agent
CC   that increases or decreases the expression of the polynucleotide sequence
CC   that is differentially expressed in neuronal tissue of a first animal
CC   subjected to pain, a method for identifying a compound which regulates
CC   the expression of a polynucleotide sequence which is differentially
CC   expressed in an animal subjected to pain, a method for identifying a
CC   compound that regulates the activity of one or more of the
CC   polynucleotides, a method for producing a pharmaceutical composition, a
CC   method for identifying a compound or small molecule that regulates the
CC   activity in an animal of one or more of the polypeptides given in the
CC   specification, a method for identifying a compound useful in treating
CC   pain and a pharmaceutical composition comprising the one or more
CC   polypeptides or their antibodies. The polynucleotide or the compound that
CC   modulates its activity is useful for preparing a medicament for treating
CC   pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC   injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC   therapy). The sequence presented is a human protein (shown in Table 2 of
CC   the specification) which is differentially expressed during pain. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic form directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 354 AA;

  Query Match           100.0%;  Score 57;  DB 7;  Length 354;
  Best Local Similarity  100.0%;  Pred. No. 0.06;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        345 KNNLKDCGLF 354


RESULT 26
ADE59391
ID   ADE59391 standard; protein; 354 AA.
XX
AC   ADE59391;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human Protein P04899, SEQ ID NO 5285.
XX
KW   Human; pain; neuronal tissue; gene therapy;
KW   spinal segmental nerve injury; chronic constriction injury; CCI;
KW   spared nerve injury; SNI; Chung.
XX
OS   Homo sapiens.
XX
PN   WO2003016475-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US025765.
XX
PR   14-AUG-2001; 2001US-0312147P.
PR   01-NOV-2001; 2001US-0346382P.
PR   26-NOV-2001; 2001US-0333347P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
XX
PI   Woolf C,  D'urso D,  Befort K,  Costigan M;
XX
DR   WPI; 2003-268312/26.
DR   GENBANK; P04899.
XX
PT   New composition comprising two or more isolated polypeptides, useful for
PT   preparing a medicament for treating pain in an animal.
XX
PS   Claim 1; Page; 1017pp; English.
XX
CC   The invention discloses a composition comprising two or more isolated rat
CC   or human polynucleotides or a polynucleotide which represents a fragment,
CC   derivative or allelic variation of the nucleic acid sequence. Also
CC   claimed are a vector comprising the novel polynucleotide, a host cell
CC   comprising the vector, a method for identifying a nucleotide sequence
CC   which is differentially regulated in an animal subjected to pain and a
CC   kit to perform the method, an array, a method for identifying an agent
CC   that increases or decreases the expression of the polynucleotide sequence
CC   that is differentially expressed in neuronal tissue of a first animal
CC   subjected to pain, a method for identifying a compound which regulates
CC   the expression of a polynucleotide sequence which is differentially
CC   expressed in an animal subjected to pain, a method for identifying a
CC   compound that regulates the activity of one or more of the
CC   polynucleotides, a method for producing a pharmaceutical composition, a
CC   method for identifying a compound or small molecule that regulates the
CC   activity in an animal of one or more of the polypeptides given in the
CC   specification, a method for identifying a compound useful in treating
CC   pain and a pharmaceutical composition comprising the one or more
CC   polypeptides or their antibodies. The polynucleotide or the compound that
CC   modulates its activity is useful for preparing a medicament for treating
CC   pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC   injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC   therapy). The sequence presented is a human protein (shown in Table 2 of
CC   the specification) which is differentially expressed during pain. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic form directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 354 AA;
```

Query Match 100.0%; Score 57; DB 7; Length 354;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 345 KNNLKDCGLF 354

RESULT 27
ADE59385
ID ADE59385 standard; protein; 354 AA.
XX
AC ADE59385;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein P04897, SEQ ID NO 5279.
XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; P04897.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 354 AA;

Query Match 100.0%; Score 57; DB 7; Length 354;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 345 KNNLKDCGLF 354

RESULT 28
ADE59389
ID ADE59389 standard; protein; 354 AA.
XX
AC ADE59389;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein P04897, SEQ ID NO 5283.
XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; P04897.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction

CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 354 AA;

Query Match 100.0%; Score 57; DB 7; Length 354;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 345 KNNLKDCGLF 354

RESULT 29
ADD46017
ID ADD46017 standard; protein; 354 AA.
XX
AC ADD46017;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein P04899, SEQ ID NO 11689.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; P04899.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 354 AA;

Query Match 100.0%; Score 57; DB 7; Length 354;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 345 KNNLKDCGLF 354

RESULT 30
ADN06138
ID ADN06138 standard; protein; 354 AA.
XX
AC ADN06138;
XX
DT 01-JUL-2004 (first entry)
XX
DE Rat Gi1 alpha subunit protein.
XX
KW G protein; alpha subunit; physiological response; neurotransmitter;
KW sensory stimuli; rat; Gi1 alpha subunit.
XX
OS Rattus sp.
XX
PN US2004072157-A1.
XX
PD 15-APR-2004.
XX
PF 31-JAN-2002; 2002US-00059266.
XX
PR 31-JAN-2001; 2001US-0265068P.
XX
PA (GRAB/) GRABER S G.
XX
PI Graber SG;
XX
DR WPI; 2004-328563/30.
DR N-PSDB; ADN06137.
XX
PT New chimeric approximatelya subunit of G proteins that affect receptor
PT coupling of the G proteins, useful in mediating an array of physiological
PT responses initiated by hormones, neurotransmitters and sensory stimuli.
XX
PS Disclosure; SEQ ID NO 4; 68pp; English.
XX
CC The invention relates to chimeric alpha subunit of G proteins. The
CC chimeric alpha subunit of G proteins is useful in mediating an array of
CC physiological responses initiated by hormones, neurotransmitters, sensory
CC stimuli and other signalling molecules. The present sequence is rat Gi1
CC alpha subunit protein.
XX
SQ Sequence 354 AA;

Query Match 100.0%; Score 57; DB 8; Length 354;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||

```
Db        345 KNNLKDCGLF 354


RESULT 31
ADQ08808
ID   ADQ08808 standard; protein; 354 AA.
XX
AC   ADQ08808;
XX
DT   26-AUG-2004  (first entry)
XX
DE   Ciona intestinalis nervous system associated protein SeqID210.
XX
KW   gene cluster; nervous system; sea-squirt tailbud; embryo; larva;
KW   nervous system disease.
XX
OS   Ciona intestinalis.
XX
PN   JP2004057127-A.
XX
PD   26-FEB-2004.
XX
PF   31-JUL-2002; 2002JP-00222532.
XX
PR   31-JUL-2002; 2002JP-00222532.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2004-208712/20.
DR   N-PSDB; ADQ08807.
XX
PT   Novel genes derived from Ciona intestinalis (sea squirt), expressed in
PT   nervous system in the tailbud embryo or larva, useful for studying the
PT   development of nervous system.
XX
PS   Claim 4; SEQ ID NO 210; 897pp; Japanese.
XX
CC   This invention relates to a novel gene cluster, where the encoded
CC   proteins are expressed in the nervous system of sea-squirt tailbud embryo
CC   or larva. The invention is useful for studying the development of the
CC   nervous system of the sea-squirt and for research purposes. The genes may
CC   be used for determining the disease-development mechanisms in the nervous
CC   system. In addition, novel gene clusters expressed in nervous system of
CC   sea-squirt tailbud embryo or larva allows development of diagnostics and
CC   therapeutics related to nervous system diseases. The present sequence is
CC   that of a protein encoded by a C intestinalis gene of the invention.
XX
SQ   Sequence 354 AA;

  Query Match             100.0%;  Score 57;  DB 8;  Length 354;
  Best Local Similarity   100.0%;  Pred. No. 0.06;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        345 KNNLKDCGLF 354


RESULT 32
AAY85149
ID   AAY85149 standard; protein; 355 AA.
XX
AC   AAY85149;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Human G-alpha-i2 amino acid sequence.
XX
KW   G-alpha-i2; antisense inhibitor; infection; inflammation; prevent;
KW   tumour formation; treatment; inhibit.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 343
FT                   /label= unknown
FT                   /note= "Encoded by GNC"
XX
PN   US6040179-A.
XX
PD   21-MAR-2000.
XX
PF   25-JUN-1999;   99US-00339993.
XX
PR   25-JUN-1999;   99US-00339993.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM;
XX
DR   WPI; 2000-270140/23.
DR   N-PSDB; AAA09737.
XX
PT   Novel antisense oligonucleotide containing compounds, useful for
PT   inhibiting the expression of G-alpha-i2 in human cells and tissues and
PT   treating infection, inflammation and cancer.
XX
PS   Example 13; Col 43-46; 31pp; English.
XX
CC   This sequence represents the human G-alpha-i2 amino acid sequence. G-
CC   alpha-i2 is a member of the Gi subfamily of G proteins, which is involved
CC   in hormonal inhibition of adenylyl cyclase and in the regulation of
CC   plasma membrane enzymes. The expression of G-alpha-i2 has been shown to
CC   be altered in some tumours. Mice lacking the G-alpha-i2 gene display
CC   growth retardation and develop adenocarcinoma of the colon and a form of
CC   lethal diffuse colitis similar to ulcerative colitis in humans. The
CC   invention relates to antisense inhibitory oligonucleotide sequences,
CC   which target the human G-alpha-i2 nucleotide sequence. The antisense
CC   molecules are useful for inhibiting the expression of G-alpha-i2 in human
CC   cells or tissues, and for treating and preventing various disorders such
CC   as infection, inflammation and tumour formation. The antisense
CC   oligonucleotides are also useful for research and diagnostic purposes
XX
SQ   Sequence 355 AA;

  Query Match             100.0%;  Score 57;  DB 3;  Length 355;
  Best Local Similarity   100.0%;  Pred. No. 0.061;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        346 KNNLKDCGLF 355


RESULT 33
AAB99065
ID   AAB99065 standard; protein; 355 AA.
XX
AC   AAB99065;
XX
DT   23-AUG-2001  (first entry)
XX
DE   Human G-protein alpha subunit i2.
XX
KW   G-protein coupled receptor; GPCR; GnRH receptor; disease treatment;
KW   gonadotrophin releasing; hormone receptor; hormone dependent cancer;
KW   human; catfish; goldfish; cow; sheep; horse; fruitfly; pig; rat; mouse;
KW   gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200136446-A2.
XX
PD   25-MAY-2001.
XX
PF   17-NOV-2000; 2000WO-GB004385.
```

XX
PR 17-NOV-1999; 99GB-00027215.
XX
PA (UYBR-) UNIV BRISTOL.
XX
PI Mcardle CA;
XX
DR WPI; 2001-355607/37.
XX
PT Use of a vector encoding G-protein coupled receptors for manufacturing
PT medicaments for treating cancer, diseases of cardiovascular system,
PT nervous system, digestive system, immune system, or muscle diseases.
XX
PS Disclosure; Fig 19; 78pp; English.
XX
CC The present invention describes a prodrug comprising a vector encoding a
CC G-protein coupled receptor (GPCR). This can be used in the treatment of
CC diseases, including hormone-dependent cancers, cardiovascular, nervous
CC system, digestive system, immune system, respiratory, skeletal,
CC endocrine, sensory and muscle diseases and disorders. The present
CC sequence is a protein described in the exemplification of the invention
XX
SQ Sequence 355 AA;

Query Match 100.0%; Score 57; DB 4; Length 355;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 346 KNNLKDCGLF 355

RESULT 34
ABB09274
ID ABB09274 standard; protein; 355 AA.
XX
AC ABB09274;
XX
DT 10-JUL-2002 (first entry)
XX
DE G protein-coupled receptor (GPCR) I2 SEQ ID NO:20.
XX
KW Target activated nucleic acid biosensor; signalling moiety; GPCR;
KW nucleic acid sensor; detection; engineering; drug optimisation;
KW G protein-coupled receptor.
XX
OS Homo sapiens.
XX
PN WO200222882-A2.
XX
PD 21-MAR-2002.
XX
PF 13-SEP-2001; 2001WO-US028835.
XX
PR 13-SEP-2000; 2000US-0232454P.
XX
PA (ARCH-) ARCHEMIX CORP.
XX
PI Stanton M, Epstein D, Hamaguchi N;
XX
DR WPI; 2002-393977/42.
XX
PT Nucleic acid sensor for detecting target molecule, comprises target
PT molecule activation site and optical signaling unit that changes its
PT optical properties upon allosteric modulation sensor after recognition of
PT target.
XX
PS Example 12; Page 89; 144pp; English.
XX
CC The present invention describes a nucleic acid sensor molecule (I)
CC comprising a target molecule activation site comprising a structure that
CC recognises a target molecule and an optical signalling unit including at
CC least one nucleotide coupled to a signalling moiety that changes its
CC optical properties upon allosteric modulation of (I) following
CC recognition of the target molecule. (I) is useful for detecting a target
CC molecule associated with a pathological condition or genetic alteration.
CC (I) is useful for identifying a drug compound, by identifying a nucleic
CC acid biosensor-based molecule profile of target molecules associated with
CC a disease trait in a patient, administering a candidate compound to the
CC patient, and monitoring changes in the profile. Alternately, the method
CC involves identifying a number of pathway target molecules, administering
CC a candidate compound to a patient having a disease trait, and monitoring
CC changes in the structure, level or activity of two or more of the pathway
CC target molecules using (I). The profile of target molecules or the
CC changes in the structure is compared to the profile of a reference
CC healthy or diseased population. (I) is useful in multiple assays, for the
CC detection of target molecule. (I) is also useful in diagnostic
CC applications and drug optimisation. The present sequence represents a G
CC protein-coupled receptor, which is used in an example from the present
CC invention
XX
SQ Sequence 355 AA;

Query Match 100.0%; Score 57; DB 5; Length 355;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 346 KNNLKDCGLF 355

RESULT 35
ABB09277
ID ABB09277 standard; protein; 355 AA.
XX
AC ABB09277;
XX
DT 10-JUL-2002 (first entry)
XX
DE G protein-coupled receptor (GPCR) g02 SEQ ID NO:23.
XX
KW Target activated nucleic acid biosensor; signalling moiety; GPCR;
KW nucleic acid sensor; detection; engineering; drug optimisation;
KW G protein-coupled receptor.
XX
OS Homo sapiens.
XX
PN WO200222882-A2.
XX
PD 21-MAR-2002.
XX
PF 13-SEP-2001; 2001WO-US028835.
XX
PR 13-SEP-2000; 2000US-0232454P.
XX
PA (ARCH-) ARCHEMIX CORP.
XX
PI Stanton M, Epstein D, Hamaguchi N;
XX
DR WPI; 2002-393977/42.
XX
PT Nucleic acid sensor for detecting target molecule, comprises target
PT molecule activation site and optical signaling unit that changes its
PT optical properties upon allosteric modulation sensor after recognition of
PT target.
XX
PS Example 12; Page 89; 144pp; English.
XX
CC The present invention describes a nucleic acid sensor molecule (I)
CC comprising a target molecule activation site comprising a structure that
CC recognises a target molecule and an optical signalling unit including at
CC least one nucleotide coupled to a signalling moiety that changes its
CC optical properties upon allosteric modulation of (I) following
CC recognition of the target molecule. (I) is useful for detecting a target

CC molecule associated with a pathological condition or genetic alteration.
CC (I) is useful for identifying a drug compound, by identifying a nucleic
CC acid biosensor-based molecule profile of target molecules associated with
CC a disease trait in a patient, administering a candidate compound to the
CC patient, and monitoring changes in the profile. Alternately, the method
CC involves identifying a number of pathway target molecules, administering
CC a candidate compound to a patient having a disease trait, and monitoring
CC changes in the structure, level or activity of two or more of the pathway
CC target molecules using (I). The profile of target molecules or the
CC changes in the structure is compared to the profile of a reference
CC healthy or diseased population. (I) is useful in multiple assays, for the
CC detection of target molecule. (I) is also useful in diagnostic
CC applications and drug optimisation. The present sequence represents a G
CC protein-coupled receptor, which is used in an example from the present
CC invention
XX
SQ Sequence 355 AA;

Query Match 100.0%; Score 57; DB 5; Length 355;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 346 KNNLKDCGLF 355

RESULT 36
AAU79335
ID AAU79335 standard; protein; 355 AA.
XX
AC AAU79335;
XX
DT 02-JUL-2002 (first entry)
XX
DE Human inhibitory G protein alpha i2.
XX
KW Human; inhibitory G protein alpha i2; antiarrhythmic; cardiant;
KW gene therapy; cardiac arrhythmia; ventricular arrythmia; syncope;
KW atrial arrhythmia; sinus bradycardia; sinus tachycardia;
KW atrial tachycardia; atrial fibrillation; atrial flutter;
KW atrioventricular nodal block; atrioventricular node reentry tachycardia;
KW atrioventricular reciprocating tachycardia; ventricular tachycardia;
KW ventricular fibrillation; sick sinus syndrome; Stokes-Adams attack;
KW chronic fatigue syndrome; cardiomyopathy.
XX
OS Homo sapiens.
XX
PN WO200219966-A2.
XX
PD 14-MAR-2002.
XX
PF 06-SEP-2001; 2001WO-US027623.
XX
PR 06-SEP-2000; 2000US-0230311P.
PR 05-JUN-2001; 2001US-0295889P.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Donahue JK, Marban E;
XX
DR WPI; 2002-329822/36.
DR N-PSDB; ABK48300, ABK48301, ABK48302, ABK48303, ABK48304, ABK48305,
DR ABK48306, ABK48307, ABK48308.
XX
PT Preventing or treating cardiac arrhythmia, e.g. atrial fibrillation,
PT comprises administering at least one polynucleotide capable of modulating
PT electrical property in standard cardiac electrophysiological assay.
XX
PS Disclosure; Fig 9A; 63pp; English.
XX
CC The invention describes a method of preventing or treating cardiac
CC arrhythmia comprising administering to a mammal at least one
CC polynucleotide capable of modulating an electrical property in a standard
CC cardiac electrophysiological assay, and expressing the polynucleotide to
CC prevent or treat the cardiac arrhythmia. The method is useful for
CC treating or preventing a wide range of ventricular or atrial arrhythmia,
CC including, sinus bradycardia (indications of which include sick sinus
CC syndrome, Stokes-Adams attacks, syncope, chronic fatigue syndrome and
CC cardiomyopathies) , sinus tachycardia, atrial tachycardia, atrial
CC fibrillation, atrial flutter, atrioventricular nodal block,
CC atrioventricular node reentry tachycardia, atrioventricular reciprocating
CC tachycardia, ventricular tachycardia or ventricular fibrillation. The new
CC method of treating cardiac arrhythmia: is genetically and spatially
CC controllable, i.e. they provide for administration of at least one pre-
CC defined polynucleotide to an identified heart tissue or focal area; may
CC be employed to supply the heart with one or a combination of different
CC therapeutic proteins; provides treated cells and tissue that usually
CC remain responsive to endogenous nerves and hormones; provides targeted
CC delivery to isolated regions of the heart (using highly localised gene
CC therapy); has readily detected therapeutic effects and incorporates a
CC method to rescue gene transfer-induced changes by conventional
CC electrophysiological methods. This is the amino acid sequence of the
CC human inhibitory G protein sub-unit G alpha i2, the polynucleotide
CC encoding which is used in the treatment of heart arrhythmia
XX
SQ Sequence 355 AA;

Query Match 100.0%; Score 57; DB 5; Length 355;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 346 KNNLKDCGLF 355

RESULT 37
ADC09612
ID ADC09612 standard; protein; 355 AA.
XX
AC ADC09612;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human G-protein coupled receptor-related protein, SEQ ID 23.
XX
KW Nucleic acid sensor molecule; ligase; cis-hammerhead; protein kinase;
KW human; G-protein coupled receptor.
XX
OS Homo sapiens.
XX
PN WO2003014375-A2.
XX
PD 20-FEB-2003.
XX
PF 09-AUG-2002; 2002WO-US025319.
XX
PR 09-AUG-2001; 2001US-0311378P.
PR 21-AUG-2001; 2001US-0313932P.
PR 13-SEP-2001; 2001US-00952680.
PR 13-NOV-2001; 2001US-0338186P.
PR 18-JAN-2002; 2002US-0349959P.
PR 13-MAR-2002; 2002US-0364486P.
PR 25-MAR-2002; 2002US-0367991P.
PR 04-APR-2002; 2002US-0369887P.
PR 01-MAY-2002; 2002US-0376744P.
PR 31-MAY-2002; 2002US-0385097P.
XX
PA (ARCH-) ARCHEMIX CORP.
XX
PI Stanton M, Epstein D, Hamaguchi N, Kurz M, Keefe T, Wilson C;
PI Grate D, Marshall KA, Mccauley T, Kurz J;
XX
DR WPI; 2003-300534/29.
XX

PT Nucleic acid sensor molecule, for identifying/detecting protein kinase in
PT a sample, comprises a target modulation domain which recognizes a target
PT molecule, a linker domain, a catalytic domain, and an optical signal
PT generator.
XX
PS Example 5; SEQ ID NO 23; 423pp; English.
XX
CC The present invention relates to nucleic acid sensor molecules (I), which
CC comprise a target modulation domain that recognizes a target molecule
CC (TM), a linker domain, a catalytic domain, and an optical signal
CC generating unit. The catalytic domain comprises a ligase or cis-
CC hammerhead. (I) are useful for identifying or detecting TM in a sample,
CC preferably a protein kinase in a sample. Target molecules include
CC proteins, post-translationally modified forms of proteins, peptides,
CC nucleic acids, oligosaccharides, nucleotides, metabolites, drugs, toxins,
CC biohazards, ions, carbohydrates, polysaccharides, hormones, receptors,
CC antigens, antibodies, viruses, metabolites, co-factors, drugs, dyes,
CC nutrients, growth factors, cCMP, cAMP or cGMP, protein kinase,
CC phosphorylated protein kinase, extracellular signal regulated kinase
CC (ERK), a component or product of mitogen activated protein (MAP) kinase
CC pathway, a MAP kinase pathway associated protein, an extracellular
CC component of MAP kinase pathway, a component of ERK1/2 MAP, JNK MAP or
CC P38 MAP kinase pathway, an endogenous form of MAP kinase (MEK), MAP
CC kinase kinase, or MAP kinase (MEKKK), or RAF kinase, Ras protein,
CC phosphatase, GTP binding protein, G-protein coupled receptor (GPCR),
CC cytokine, growth factor, cellular metabolite, small molecule or lysozyme.
CC (I) are also useful for identifying a modulator of protein kinase
CC activity. In an example from the invention, nucleic acid sensor molecules
CC which signal human G-protein coupled receptors e.g. the present sequence,
CC were obtained.
XX
SQ Sequence 355 AA;

Query Match 100.0%; Score 57; DB 7; Length 355;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 346 KNNLKDCGLF 355

RESULT 38
ADC09609
ID ADC09609 standard; protein; 355 AA.
XX
AC ADC09609;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human G-protein coupled receptor-related protein, SEQ ID 20.
XX
KW Nucleic acid sensor molecule; ligase; cis-hammerhead; protein kinase;
KW human; G-protein coupled receptor.
XX
OS Homo sapiens.
XX
PN WO2003014375-A2.
XX
PD 20-FEB-2003.
XX
PF 09-AUG-2002; 2002WO-US025319.
XX
PR 09-AUG-2001; 2001US-0311378P.
PR 21-AUG-2001; 2001US-0313932P.
PR 13-SEP-2001; 2001US-00952680.
PR 13-NOV-2001; 2001US-0338186P.
PR 18-JAN-2002; 2002US-0349959P.
PR 13-MAR-2002; 2002US-0364486P.
PR 25-MAR-2002; 2002US-0367991P.
PR 04-APR-2002; 2002US-0369887P.
PR 01-MAY-2002; 2002US-0376744P.
PR 31-MAY-2002; 2002US-0385097P.
XX
PA (ARCH-) ARCHEMIX CORP.
XX
PI Stanton M, Epstein D, Hamaguchi N, Kurz M, Keefe T, Wilson C;
PI Grate D, Marshall KA, Mccauley T, Kurz J;
XX
DR WPI; 2003-300534/29.
XX
PT Nucleic acid sensor molecule, for identifying/detecting protein kinase in
PT a sample, comprises a target modulation domain which recognizes a target
PT molecule, a linker domain, a catalytic domain, and an optical signal
PT generator.
XX
PS Example 5; SEQ ID NO 20; 423pp; English.
XX
CC The present invention relates to nucleic acid sensor molecules (I), which
CC comprise a target modulation domain that recognizes a target molecule
CC (TM), a linker domain, a catalytic domain, and an optical signal
CC generating unit. The catalytic domain comprises a ligase or cis-
CC hammerhead. (I) are useful for identifying or detecting TM in a sample,
CC preferably a protein kinase in a sample. Target molecules include
CC proteins, post-translationally modified forms of proteins, peptides,
CC nucleic acids, oligosaccharides, nucleotides, metabolites, drugs, toxins,
CC biohazards, ions, carbohydrates, polysaccharides, hormones, receptors,
CC antigens, antibodies, viruses, metabolites, co-factors, drugs, dyes,
CC nutrients, growth factors, cCMP, cAMP or cGMP, protein kinase,
CC phosphorylated protein kinase, extracellular signal regulated kinase
CC (ERK), a component or product of mitogen activated protein (MAP) kinase
CC pathway, a MAP kinase pathway associated protein, an extracellular
CC component of MAP kinase pathway, a component of ERK1/2 MAP, JNK MAP or
CC P38 MAP kinase pathway, an endogenous form of MAP kinase (MEK), MAP
CC kinase kinase, or MAP kinase (MEKKK), or RAF kinase, Ras protein,
CC phosphatase, GTP binding protein, G-protein coupled receptor (GPCR),
CC cytokine, growth factor, cellular metabolite, small molecule or lysozyme.
CC (I) are also useful for identifying a modulator of protein kinase
CC activity. In an example from the invention, nucleic acid sensor molecules
CC which signal human G-protein coupled receptors e.g. the present sequence,
CC were obtained.
XX
SQ Sequence 355 AA;

Query Match 100.0%; Score 57; DB 7; Length 355;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 346 KNNLKDCGLF 355

RESULT 39
ADJ68621
ID ADJ68621 standard; protein; 355 AA.
XX
AC ADJ68621;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human heat mitochondrial protein as a therapeutic target SeqID427.
XX
KW mitochondrial; human; screening assay; diabetes mellitus;
KW Huntington's disease; osteoarthritis;
KW Leber's hereditary optic neuropathy; LHON;
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW osteopathic; ophthalmological; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2003087768-A2.
XX
PD 23-OCT-2003.

```
XX
PF   04-APR-2003; 2003WO-US010870.
XX
PR   12-APR-2002; 2002US-0372843P.
PR   17-JUN-2002; 2002US-0389987P.
PR   20-SEP-2002; 2002US-0412418P.
XX
PA   (MITO-) MITOKOR.
PA   (BUCK-) BUCK INST AGE RES.
XX
PI   Ghosh SS,  Fahy ED,  Zhang B,  Gibson BW,  Taylor SW,  Glenn GM;
PI   Warnock DE;
XX
DR   WPI; 2003-845369/78.
XX
PT   Identifying a mitochondrial target for drug screening assays and for
PT   treating diseases associated with altered mitochondrial function,
PT   comprises detecting a modified polypeptide in a sample and correlating
PT   with the disease.
XX
PS   Claim 1; SEQ ID NO 427; 180pp; English.
XX
CC   This invention relates to novel mitochondrial targets that can be used
CC   for therapeutic intervention in treating a disease associated with
CC   altered mitochondrial function. Specifically, it refers to a method for
CC   identifying proteins of the human heart mitochondrial proteome that are
CC   useful for drug screening assays, as well as therapeutic targets. The
CC   present invention describes a method for identifying such proteins that
CC   can be used in the treatment of various diseases associated with altered
CC   mitochondrial function including diabetes mellitus, Huntington's disease,
CC   osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC   encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC   ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC   compositions have neuroprotective, nootropic, antidiabetic,
CC   anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC   cytostatic activities. This polypeptide sequence is a human heart
CC   mitochondrial protein of the invention.
XX
SQ   Sequence 355 AA;

  Query Match             100.0%;  Score 57;  DB 7;  Length 355;
  Best Local Similarity   100.0%;  Pred. No. 0.061;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        346 KNNLKDCGLF 355


RESULT 40
ADJ70586
ID   ADJ70586 standard; protein; 355 AA.
XX
AC   ADJ70586;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Human heat mitochondrial protein as a therapeutic target SeqID2392.
XX
KW   mitochondrial; human; screening assay; diabetes mellitus;
KW   Huntington's disease; osteoarthritis;
KW   Leber's hereditary optic neuropathy; LHON;
KW   mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW   myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW   neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW   osteopathic; ophthalmological; cytostatic.
XX
OS   Homo sapiens.
XX
PN   WO2003087768-A2.
XX
PD   23-OCT-2003.
XX
PF   04-APR-2003; 2003WO-US010870.
XX
PR   12-APR-2002; 2002US-0372843P.
PR   17-JUN-2002; 2002US-0389987P.
PR   20-SEP-2002; 2002US-0412418P.
XX
PA   (MITO-) MITOKOR.
PA   (BUCK-) BUCK INST AGE RES.
XX
PI   Ghosh SS,  Fahy ED,  Zhang B,  Gibson BW,  Taylor SW,  Glenn GM;
PI   Warnock DE;
XX
DR   WPI; 2003-845369/78.
XX
PT   Identifying a mitochondrial target for drug screening assays and for
PT   treating diseases associated with altered mitochondrial function,
PT   comprises detecting a modified polypeptide in a sample and correlating
PT   with the disease.
XX
PS   Claim 1; SEQ ID NO 2392; 180pp; English.
XX
CC   This invention relates to novel mitochondrial targets that can be used
CC   for therapeutic intervention in treating a disease associated with
CC   altered mitochondrial function. Specifically, it refers to a method for
CC   identifying proteins of the human heart mitochondrial proteome that are
CC   useful for drug screening assays, as well as therapeutic targets. The
CC   present invention describes a method for identifying such proteins that
CC   can be used in the treatment of various diseases associated with altered
CC   mitochondrial function including diabetes mellitus, Huntington's disease,
CC   osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC   encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC   ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC   compositions have neuroprotective, nootropic, antidiabetic,
CC   anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC   cytostatic activities. This polypeptide sequence is a human heart
CC   mitochondrial protein of the invention.
XX
SQ   Sequence 355 AA;

  Query Match             100.0%;  Score 57;  DB 7;  Length 355;
  Best Local Similarity   100.0%;  Pred. No. 0.061;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNNLKDCGLF 10
              ||||||||||
Db        346 KNNLKDCGLF 355


RESULT 41
ADP70781
ID   ADP70781 standard; protein; 355 AA.
XX
AC   ADP70781;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Minicell related human G i protein.
XX
KW   minicell; eukaryotic; archaebacterial; organellar membrane protein;
KW   fusion; transmembrane; membrane-anchoring domain; vaccination;
KW   drug discovery; proteomics.
XX
OS   Homo sapiens.
OS   Unidentified.
XX
PN   WO2003072014-A2.
XX
PD   04-SEP-2003.
XX
PF   28-MAY-2002; 2002WO-US016877.
XX
PR   25-FEB-2002; 2002US-0359843P.
PR   24-MAY-2002; 2002US-00154951.
```

XX
PA (MPEX-) MPEX BIOSCIENCE INC.
XX
PI Sabbadini RA, Surber M, Berkley N, Segall A, Klepper R;
PI Giacalone M, Gerhart W;
XX
DR WPI; 2003-833248/77.
DR N-PSDB; ADP70682.
XX
PT New minicells containing specific membrane proteins, useful e.g. for
PT delivering therapeutic or diagnostic agents, in drug screening and for
PT protein production.
XX
PS Disclosure; Page 532-535; 669pp; English.
XX
CC The invention relates to a novel minicell that includes a eukaryotic,
CC archaebacterial or organellar membrane protein. The invention further
CC comprises: a minicell that includes: a membrane protein fusion consisting
CC of a polypeptide with at least one transmembrane or membrane-anchoring
CC domain and a second polypeptide not derived from eubacterial protein and
CC being neither a His tag nor a glutathione-S-transferase polypeptide; or a
CC membrane conjugate, comprising membrane protein chemically linked to a
CC compound or a biologically active compound; displays a synthetic linkage
CC group, (non-)covalently attached to a membrane component; is sterically
CC stabilised with half-life in vivo longer than the wild type; includes an
CC expression cassette comprising an open reading frame that encodes the
CC membrane protein; includes at least one nucleic acid and displays a
CC binding group for a target; includes a nucleic acid that contains both
CC eukaryotic and eubacterial expression sequences, independently linked to
CC an open reading frame; includes two nucleic acids, one with eukaryotic
CC and the other with eubacterial expression sequences, linked to different
CC open reading frames; contains a crystal of the membrane protein; or
CC displays a binding group and can selectively absorb and/or internalise an
CC undesirable compound; producing the minicells; a poroplast comprising a
CC vesicle, bordered by a eubacterial inner membrane, that is accessible to
CC a compound present in solution with the poroplast, surrounded by a
CC eubacterial cell wall; producing (cellular) poroplasts; a solid support
CC carrying a minicell; a device comprising: a microchip, associated with a
CC biosensor and comprising, or contacting, a minicell that displays the
CC binding group; or microchips, associated with a biosensor and comprising
CC sets of minicells, in a known pattern, that display different targets; a
CC library of minicells that express different exogenous proteins, different
CC fusion proteins or a constant protein and a variable protein; a parent
CC cell that produces minicells; and using minicells. These processes are
CC used for a wide range of diagnostic and (gene) therapeutic procedures
CC (including vaccination), also for drug discovery, functional proteomics
CC and research. This seqeunce represents a protein derived from a DNA
CC sequence used in the construction of a minicell of the invention.
XX
SQ Sequence 355 AA;

Query Match 100.0%; Score 57; DB 7; Length 355;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 346 KNNLKDCGLF 355

RESULT 42
ADM67196
ID ADM67196 standard; protein; 355 AA.
XX
AC ADM67196;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human adipocyte specific G-protein alpha inhibiting 1 protein SeqID 550.
XX
KW human; adipocyte specific; adipose tissue; anti-obesity;
KW high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes;
KW adipogenesis; hypertension; cardiovascular disease; anorectic;
KW antidiabetic; hypotensive; G-protein alpha inhibiting 1.
XX
OS Homo sapiens.
XX
PN WO2004011618-A2.
XX
PD 05-FEB-2004.
XX
PF 29-JUL-2003; 2003WO-US023684.
XX
PR 29-JUL-2002; 2002US-0398785P.
PR 12-JUN-2003; 2003US-0478206P.
XX
PA (HMGE-) HMGENE INC.
XX
PI Chada K, Chouinard R, Ashar H, Sayed AMD;
XX
DR WPI; 2004-143846/14.
DR N-PSDB; ADM66917.
XX
PT Identifying adipocyte specific genes, useful for treating obesity or
PT diabetes, and for identifying drug targets, by differential gene
PT expression analysis between adipose tissue or stromal vascular tissue of
PT mice of different genotypes.
XX
PS Disclosure; SEQ ID NO 550; 91pp; English.
XX
CC This invention relates to a novel method for identifying genes that are
CC over-expressed in adipose tissue and as such it provides targets for anti
CC -obesity pharmaceutical compositions. Specifically, it refers to a high
CC mobility group I-C protein (HMGI-C) that is associated with obesity and
CC is epistatic to leptin, furthermore, it refers to the ob gene where an
CC autosomal recessive trait is linked to obesity and diabetes. The present
CC invention describes performing differential gene expression analysis
CC between the white adipose tissue (WAT) or stromal vascular tissue (SVT)
CC of any two different mice selected from a group consisting of wild-type,
CC HMGI-C -/-, ob/ob, or HMGI-C -/- ob/ob genotype mice. Accordingly, using
CC this method novel nucleotides and the encoded proteins thereof were
CC identified that are adipocyte specific, and as such can be used for
CC preventing adipogenesis, diagnosing and treating diabetes, obesity,
CC hypertension and cardiovascular disease, as well as screening for
CC compounds that can modulate or prevent adipogenesis and treat diabetes or
CC obesity. These compositions exhibit anorectic, antidiabetic and
CC hypotensive activities. This polypeptide sequence is a human homologue of
CC a murine adipocyte specific protein sequence of the invention.
XX
SQ Sequence 355 AA;

Query Match 100.0%; Score 57; DB 8; Length 355;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 346 KNNLKDCGLF 355

RESULT 43
ABM80456
ID ABM80456 standard; protein; 355 AA.
XX
AC ABM80456;
XX
DT 18-NOV-2004 (first entry)
XX
DE Tumour-associated antigenic target (TAT) polypeptide PRO71103, SEQ:1148.
XX
KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;

KW gene therapy; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2004030615-A2.
XX
PD 15-APR-2004.
XX
PF 29-SEP-2003; 2003WO-US028547.
XX
PR 02-OCT-2002; 2002US-0414971P.
XX
PA (GETH) GENENTECH INC.
XX
PI Wu TD, Zhang Z, Zhou Y;
XX
DR WPI; 2004-347921/32.
DR N-PSDB; ACN37935.
XX
PT New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.
XX
PS Claim 12; SEQ ID NO 1148; 7273pp; English.
XX
CC The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antagonists, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAT polypeptide of the invention
XX
SQ Sequence 355 AA;

Query Match 100.0%; Score 57; DB 8; Length 355;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 346 KNNLKDCGLF 355

RESULT 44
ADG36979
ID ADG36979 standard; protein; 362 AA.
XX
AC ADG36979;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human GPCR Gi2 alpha-Hisx6 fusion protein.
XX
KW Human; GPCR; G protein-coupled receptor; C-PLACE 1003238; G16 alpha;
KW Gi2 alpha; uropathic; gynaecological; GDP/GTP exchange reaction;
KW urinary tract disease; placental disease; tonsil disease;
KW Hisx6 fusion protein.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN JP2003232790-A.
XX
PD 22-AUG-2003.
XX
PF 12-FEB-2002; 2002JP-00034569.
XX
PR 12-FEB-2002; 2002JP-00034569.
XX
PA (SUMU) SUMITOMO SEIYAKU KK.
XX
DR WPI; 2004-014845/02.
DR N-PSDB; ADG36978.
XX
PT Ligand screening system comprising a component which is a lipid bilayer
PT membrane that contains C-PLACE1003238 and a region concerned in binding
PT of G-protein.
XX
PS Example 1; SEQ ID NO 17; 28pp; Japanese.
XX
CC The invention relates to a screening system of a ligand with respect to C
CC -PLACE1003238 (a GPCR), where a ligand-receptor interaction promotes
CC activity of GDP or GTP exchange reaction of G-protein subunits comprises,
CC a component which is a lipid bilayer membrane that contains a polypeptide
CC having a region which is concerned in binding with guanine nucleotide in
CC G protein-coupling receptor (GPCR) of the G-protein alpha (G16 alpha or
CC Gi2 alpha) subunit that belongs to the Gi family. Also included are
CC screening a ligand (involving comparing the effect of effector when
CC interacted with ligand in presence or absence of the test material),
CC producing a prophylactic and therapeutic agent of diseases of the urinary
CC tract, placenta or tonsil (involving mixing the effector and a carrier),
CC identifying a marker substance of the disease in the urinary tract,
CC placenta or tonsil (involving comparing the presence of ligand identified
CC in the biological sample derived tonsils obtained from patients and
CC normal humans), diagnosing disease in urinary tract, placenta or tonsil
CC and an antibody recognising the peptide which consists of amino acids 12-
CC 36 of C-PLACE1003238. The screening system is useful for screening for
CC the ligand which is useful in treating and preventing the disease in the
CC tissue of urinary organ, placenta or tonsil. The present sequence is a
CC Human GPCR Gi2 alpha-Hisx6 fusion protein used in the screening method of
CC the invention.
XX
SQ Sequence 362 AA;

Query Match 100.0%; Score 57; DB 8; Length 362;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 353 KNNLKDCGLF 362

RESULT 45
ABR56305
ID ABR56305 standard; protein; 695 AA.
XX
AC ABR56305;
XX
DT 20-NOV-2003 (first entry)
XX
DE pc901HISGalphai2 protein.
XX
KW Human; anorectic; antidiabetic; antilipemic; hypothalamus;
KW G-protein coupled receptor 901; obesity; diabetes; hyperlipaemia;
KW cibophobia; anorexia nervosa.
XX
OS Unidentified.
XX
PN WO2003030936-A1.
XX

PD 17-APR-2003.
XX
PF 02-OCT-2002; 2002WO-JP010250.
XX
PR 02-OCT-2001; 2001JP-00306872.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
XX
PI Sugaru E, Tsuchida A, Yamanaka M, Taiji M;
XX
DR WPI; 2003-354886/33.
DR N-PSDB; ACC70860.
XX
PT Inhibitors of expression or activity of G-protein coupled receptor 901
PT for treatment of lifestyle-related diseases and cibophobia.
XX
PS Disclosure; Page 79-81; 91pp; Japanese.
XX
CC The present invention relates to novel remedies for the treatment of
CC diseases containing as an active component an inhibitor of the expression
CC or activity of hypothalamus-expressed G-protein coupled receptor 901 and
CC for treatment of cibophobia containing as an active component a
CC potentiator of the expression or activity of G-protein coupled receptor
CC 901. The diseases which can be treated include obesity, diabetes and
CC hyperlipaemia, and cibophobia (anorexia nervosa). The present sequence
CC was used to illustrate the invention
XX
SQ Sequence 695 AA;

Query Match 100.0%; Score 57; DB 6; Length 695;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 686 KNNLKDCGLF 695

RESULT 46
ABB56396
ID ABB56396 standard; protein; 709 AA.
XX
AC ABB56396;
XX
DT 18-FEB-2002 (first entry)
XX
DE TSHR-Gs-alpha fusion protein, SEQ ID NO: 589.
XX
KW Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
KW constitutively activated GPCR; TSHR-Gs-alpha; TSHR-Gi-alpha; fusion;
KW TSHR; thyroid stimulating hormone receptor; agonist; disease.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200177172-A2.
XX
PD 18-OCT-2001.
XX
PF 05-APR-2001; 2001WO-US011098.
XX
PR 07-APR-2000; 2000US-0195747P.
XX
PA (AREN-) ARENA PHARM INC.
XX
PI Lehmann-Bruinsma K, Liaw CW, Lin I;
XX
DR WPI; 2001-648759/74.
DR N-PSDB; ABI90836.
XX
PT Identifying agonists of G protein-coupled receptors (GPCRs) for use in
PT disease treatment, comprises contacting candidate compounds with versions
PT of GPCRs.
XX
PS Example 6; Page 392-394; 394pp; English.
XX
CC The invention relates to G protein-coupled receptors (GPCRs) for which
CC the endogenous ligand has been identified. Non-endogenous constitutively
CC activated versions of known GPCRs are used in the invention for the
CC direct identification of candidate compounds as receptor agonists,
CC inverse agonists or partial agonists. Such agonists are useful as
CC therapeutic agents for diseases or disorders associated with GPCRs. The
CC present sequence is a GPCR fusion protein containing thyroid stimulating
CC hormone receptor (TSHR)
XX
SQ Sequence 709 AA;

Query Match 100.0%; Score 57; DB 4; Length 709;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 700 KNNLKDCGLF 709

RESULT 47
ABR55447
ID ABR55447 standard; protein; 709 AA.
XX
AC ABR55447;
XX
DT 29-JUL-2003 (first entry)
XX
DE Amino acid sequence of a endogenous MCH receptor-G protein Gi fusion.
XX
KW G-protein receptor; SLC-1; melanin concentrating hormone receptor;
KW MCH receptor; obesity; obesity related disorder; anxiety; depression;
KW diabetes; syndrome X; impaired glucose tolerance; dyslipidemia;
KW hypertension; coronary heart disease; cardiovascular disorder;
KW atherosclerosis; insulin resistance; psoriasis;
KW polycystic ovarian syndrome; renal disease; diabetic nephropathy;
KW glomerulonephritis; glomerular sclerosis; nephrotic syndrome;
KW hypertensive nephrosclerosis; microalbuminuria; eating disorder;
KW movement disorder; Parkinson's disease; Huntington's chorea; steroid;
KW pituitary hormone disorder; epinephrine release disorder;
KW anxiety disorder; gastrointestinal disorder; cardiovascular disorder;
KW electrolyte balance disorder; respiratory disorder; asthma;
KW reproductive disorder; immune disorder; endocrine disorder;
KW musculoskeletal disorder; neuroendocrine disorder; cognitive disorder;
KW memory disorder; motor coordination disorder;
KW sensory integration disorder; motor integration disorder;
KW dopaminergic function disorder; sensory transmission disorder;
KW olfaction disorder; sympathetic innervation disorder; affective disorder;
KW stress-related disorder; fluid-balance disorder; seizure disorder; pain;
KW psychotic behaviour; morphine tolerance; opiate addiction; migraine.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Protein 1. .353
FT /note= "MCH receptor"
FT Protein 356. .711
FT /note= "G protein Gi"
XX
PN WO2003028641-A2.
XX
PD 10-APR-2003.
XX
PF 30-SEP-2002; 2002WO-US031059.
XX
PR 01-OCT-2001; 2001US-0326463P.
PR 02-OCT-2001; 2001US-0326758P.
XX
PA (TAIS) TAISHO PHARM CO LTD.

XX
PI Sekiguchi Y, Kanuma K, Omodera K, Tran T, Kramer BA, Beeley NRA;
XX
DR WPI; 2003-441069/41.
DR N-PSDB; ACC70137.
XX
PT Method of modulating G-protein receptor, SLC-1 for treating e.g. obesity,
PT depression or anxiety, comprises contacting a melanin concentrating
PT hormone (MCH) receptor antagonist with the SLC-1 receptor.
XX
PS Example 3582; Page 1169-1171; 1171pp; English.
XX
CC The specification describes a method of modulating the G-protein
CC receptor, SLC-1. The method comprises contacting SLC-1 with a melanin
CC concentrating hormone (MCH) receptor antagonist. This antagonist is of a
CC formula given in the specification. Antagonists of the invention are used
CC for treatment of obesity, obesity related disorder, anxiety, or
CC depression in mammals. They are also used for treating type II diabetes,
CC syndrome X, impaired glucose tolerance; dyslipidemia, hypertension,
CC coronary heart disease and other cardiovascular disorders including
CC atherosclerosis, insulin resistance associated with obesity and
CC psoriasis, for treating diabetic complications and other diseases e.g.
CC polycystic ovarian syndrome (PCOS), renal disease e.g. diabetic
CC nephropathy, glomerulonephritis, glomerular sclerosis, nephrotic
CC syndrome, hypertensive nephrosclerosis, end-stage renal diseases and
CC microalbuminuria as well as eating disorder, movement disorder e.g.
CC Parkinson's disease, Huntington's chorea, a steroid or pituitary hormone
CC disorder, an epinephrine release disorder, anxiety disorder,
CC gastrointestinal disorder, a cardiovascular disorder, an electrolyte
CC balance disorder, a respiratory disorder, asthma, reproductive function
CC disorder, immune disorder, endocrine disorder, musculoskeletal disorder,
CC a neuroendocrine disorder, a cognitive disorder, memory disorder, sensory
CC modulation and transmission disorder, motor coordination disorder,
CC sensory integration disorder, a motor integration disorder, dopaminergic
CC function disorder, sensory transmission disorder, olfaction disorder,
CC sympathetic innervation disorder, affective disorder, stress-related
CC disorder, fluid-balance disorder, seizure disorder, pain, psychotic
CC behaviour, morphine tolerance, opiate addiction or migraine. The present
CC sequence is a fusion of endogenous human MCH receptor and G protein Gi,
CC which is used in the course of the invention
XX
SQ Sequence 709 AA;

Query Match 100.0%; Score 57; DB 6; Length 709;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 700 KNNLKDCGLF 709

RESULT 48
AAB99036
ID AAB99036 standard; protein; 725 AA.
XX
AC AAB99036;
XX
DT 24-AUG-2001 (first entry)
XX
DE Human somatostatin receptor 2/Galphai1 fusion protein.
XX
KW G-protein coupled receptor; GPCR; GnRH receptor; disease treatment;
KW gonadotrophin releasing; hormone receptor; hormone dependent cancer;
KW human; catfish; goldfish; cow; sheep; horse; fruitfly; pig; rat; mouse;
KW gene therapy.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200136446-A2.
XX
PD 25-MAY-2001.
XX
PF 17-NOV-2000; 2000WO-GB004385.
XX
PR 17-NOV-1999; 99GB-00027215.
XX
PA (UYBR-) UNIV BRISTOL.
XX
PI Mcardle CA;
XX
DR WPI; 2001-355607/37.
XX
PT Use of a vector encoding G-protein coupled receptors for manufacturing
PT medicaments for treating cancer, diseases of cardiovascular system,
PT nervous system, digestive system, immune system, or muscle diseases.
XX
PS Disclosure; Page 30-31; 78pp; English.
XX
CC The present invention describes a prodrug comprising a vector encoding a
CC G-protein coupled receptor (GPCR). This can be used in the treatment of
CC diseases, including hormone-dependent cancers, cardiovascular, nervous
CC system, digestive system, immune system, respiratory, skeletal,
CC endocrine, sensory and muscle diseases and disorders. The present
CC sequence is a protein described in the exemplification of the invention
XX
SQ Sequence 725 AA;

Query Match 100.0%; Score 57; DB 4; Length 725;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 716 KNNLKDCGLF 725

RESULT 49
ADG37260
ID ADG37260 standard; protein; 784 AA.
XX
AC ADG37260;
XX
DT 26-FEB-2004 (first entry)
XX
DE Fusion construct pc5HT1aHISGalphai2.
XX
KW screening; human; G protein coupled receptor; GPCR;
KW lipid bilayer membrane; fusion protein; G-alpha 16; G-alpha i2;
KW G-alpha S2; orphan GPCR;
KW G protein conjugation seven-transmembrane-type receptor.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN JP2003210192-A.
XX
PD 29-JUL-2003.
XX
PF 18-JAN-2002; 2002JP-00010871.
XX
PR 18-JAN-2002; 2002JP-00010871.
XX
PA (SUMU) SUMITOMO SEIYAKU KK.
XX
DR WPI; 2003-819838/77.
DR N-PSDB; ADG37257.
XX
PT Screening ligands for G protein coupled receptor comprises lipid bilayer
PT membrane containing embedded fusion protein comprising target G protein
PT coupled receptor and G alpha protein.
XX
PS Example 2; SEQ ID NO 20; 29pp; Japanese.
XX
CC This invention describes a novel system of screening for ligands of the

CC human G protein coupled receptor (GPCR). The method comprises a lipid
CC bilayer membrane in which a fusion protein comprising target GPCR and G-
CC alpha 16 or G-alpha i2 or G-alpha S2 is embedded. The invention also
CC discloses a second screening system where an orphan GPCR (G protein
CC conjugation seven-transmembrane-type receptor) is used to screen compound
CC having agonist and/or antagonist activity for the GPCR and to screen low
CC molecular non-peptide ligands. The screening is rapid and favourable.
XX
SQ Sequence 784 AA;

Query Match 100.0%; Score 57; DB 7; Length 784;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 775 KNNLKDCGLF 784

RESULT 50
ADC51269
ID ADC51269 standard; protein; 987 AA.
XX
AC ADC51269;
XX
DT 18-DEC-2003 (first entry)
XX
DE Chimeric ECFP, EGFP, G alpha i2, rapI GAPII protein.
XX
KW G protein activation; ECFP; enhanced cyan fluorescent protein; EYFP;
KW enhanced yellow fluorescent protein; G alpha i2; rapI GAPII; rat; human.
XX
OS Chimeric.
OS Synthetic.
OS Rattus sp.
OS Homo sapiens.
XX
PN JP2003024078-A.
XX
PD 28-JAN-2003.
XX
PF 18-JUL-2001; 2001JP-00218756.
XX
PR 18-JUL-2001; 2001JP-00218756.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR WPI; 2003-486383/46.
DR N-PSDB; ADC51268.
XX
PT Novel fusion polypeptide for measuring G protein activation, comprises G
PT protein alpha subunit trimer, its target protein, a fluorescent acceptor
PT protein and a fluorescent donor protein, linked to each other.
XX
PS Disclosure; SEQ ID NO 12; 20pp; Japanese.
XX
CC The invention relates to a fusion polypeptide for measuring G protein
CC activation, comprising all or a part of an amino acid sequence of G
CC protein alpha subunit trimer (Ia), a target protein (Ib) of G protein
CC alpha subunit trimer, a fluorescent acceptor protein (Ic) and a
CC fluorescent donor protein (Id), or their variant amino acid sequences,
CC linked to each other. The fusion polypeptide is useful for measuring the
CC activation of G protein trimer, in vitro or in vivo. In vivo measurement
CC of G protein trimer activation is possible using the fusion polypeptide.
CC The present sequence is used in the exemplification of the invention.
XX
SQ Sequence 987 AA;

Query Match 100.0%; Score 57; DB 7; Length 987;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKDCGLF 10
||||||||||
Db 733 KNNLKDCGLF 742

Search completed: March 22, 2005, 06:46:58
Job time : 165 secs